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(54) Title: ASSAY FOR DETECTING AND IDENTIFYING MICRO-ORGANISMS

(57) Abstract: The present invention also relates to an assay for detecting and identifying micro-organisms, and in particular bacteria. The present invention also relates to an assay for detecting micro-organisms, and in particular bacteria, in a sample, and for the discrimination thereof. More in particular the present invention relates to an assay for the molecular identification of bacteria according to Gram-, genus- species- and strain-specificity based on multigenotypic testing of bacterial DNA from human, animal or environmental samples.



Assay for detecting and identifying micro-organisms

Field of the invention

The present invention relates to an assay and a method for diagnosing and identifying micro-organisms, and in particular bacteria. The present invention also relates to an assay and a method for detecting micro-organisms, and in particular bacteria, in a sample, and for the discrimination thereof.

More in particular the present invention relates to an assay and a method for the molecular identification of bacteria according to Gram-, genus- species- and strain-specificity based on multigenotypic testing of bacterial DNA from human, animal or environmental samples.

Background

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In the medical and veterinary clinical setting, detection and species identification of harmful bacteria infecting biological fluids or tissues is a pre-requisite for appropriate and timely relevant antibiotherapy. Such identification is classically performed by conventional microbiological methods (culture on solid medium or in liquid phase). These conventional methods have however their own limitations.

Culture is always followed by phenotypic identification, which is based on the biochemical features of the bacteria. Usually, the whole process requires 48 to 72 hours to be completed. This period is unfortunately too long, considering the speed of bacterial growth in infected tissues and, for some bacteria, the pathological effects related the toxins that they produce. This time is also too long when bacteria are spread in the environment (aerosol, food or water contamination), where germs are able to infect humans or animals and spread rapidly on a epidemic way from an infected to a healthy body on a very short time. There is therefore a need for the rapid detection and identification of pathogenic bacterial agent(s) involved in human or animal infections or present in the environment.

A stream of studies carried out recently has confirmed that molecular identification is more efficient than phenotypic identification (Bosshard *et al*, 2003; Bosshard *et al*, 2004; Lecouvet *et al*, 2004) and genotypic definition of bacteria species has now become the gold standard (Clarridge, 2004). There is therefore an increasing need for identifying bacterial species with more reliable methods. While obvious in the hospital setting, it is also of interest of the post September 2001 era, where accuracy and speed in identification of deadly bacteria are priorities.

Aside of the time required for routine microbiologic detection, another limiting factor is sometimes the lack of bacterial growth, generating a false-negative microbiologic result. False-negative bacterial cultures are not unusual in the clinical practice, even when clinical and biological signs clearly suggest a florid and active infection (Lecouvet *et al*, 2004). This false-negativity may be due to a low organism burden, non-culturable or slowly growing micro-organisms or, most often, to prior antibiotic therapy (Trampuz *et al*, 2003; Tzanakaki *et al*, 2003). In this case, a false-negative result hampers correct etiological diagnosis regarding the bacterial origin of the infectious disease, and precludes the use of early targeted antibiotherapy. As delayed antibiotherapy may increase the risk of worse clinical outcome (Gutierrez *et al*, 1998; Yu *et al*, 2003, Lecouvet *et al*, 2004), this situation often prompts the use of empiric, broad spectrum and sometimes long-term therapy, and certainly when there is no microbiologic result.

The higher sensitivity, speed and accuracy of DNA amplification by PCR for identification of bacteria is expected to reduce the time to diagnosis, to improve the diagnostic rate, and to allow an early choice of specific antibiotic treatment. Over the last decade, this expectation has fuelled the development of numerous promising DNA assays for detecting and identifying bacteria at the species- or genera-level in human and environmental samples (Jonas et al, 2003; Palomares et al, 2003; Poyart et al, 2001; Xu et al, 2002).

These assays remain however restricted to single species and/or genera (Brakstad et al, 1992; Poyart et al, 2001; Vannuffel et al, 1998). Such restriction has various disadvantages. For instance, in the absence of any indication on the presence of bacterial agents in an environmental sample or in a biological tissue/fluid sample from human or animal origin suspected to be infected but showing no bacterial background due to the presence of a normal bacterial flora, molecular screening methods have to be applied which target the greatest as possible number of potentially pathogenic bacteria including the most feared bacteria (Staphylococci, Streptococci, Bacillus anthracis, Enterobacteriacea, Neisseria, etc...) that could be used by bioterrorists. In this case, the use of specific markers or well-defined genera requires multiple and/or repeated testing to confirm or exclude a bacterial diagnosis. Considering the cost of this strategy as well as the limited amount DNA usually available for one sample, this is practically impossible to be performed.

In another example, in samples from tissues showing a bacterial background due the presence of a normal flora, the identification of a well defined panel of pathogenic bacteria recognized as "prior key targets" in the clinical setting considered (e.g. community-acquired pneumonia) remains very difficult.

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In view of the above, there is therefore a need for the rapid detection and identification of pathogenic bacterial agent(s) involved in human or animal infections or present in the environment.

There is also a need for identification and diagnostic tools, which allow screening for the presence of pathogenic bacterial agent(s), and to detect and identify these pathogenic bacteria within a bacterial background.

In particular, it is clear that there is a great need in the art for molecular screening/detection and identification assays and methods having a range of specificity that is as wide as possible in order to quickly detect the presence of bacteria (bacterial detection step), while allowing in parallel or subsequently, to identify the present bacterial species, genera and, optionally the strain (bacterial identification step).

In a first aspect, the present invention therefore aims to provide an improved assay for detecting micro-organisms, and in particular bacteria. It is further an aim of the invention to provide an improved assay for diagnosing bacterial infection of a sample and/or tissue.

In another aspect, the present invention also aims to provide an improved assay and method for the identification of micro-organisms. More in particular, the invention aims to identify and provide a series of specific, molecular markers for the detection and/or identification of micro-organisms, and preferably bacteria, in a Gram-, genus- species-and/or strain-specific way.

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Summary

The present invention relates to an assay for detecting and identifying one or more micro-organisms in a sample, characterized in that said assay comprises the use of at least two conserved molecular markers. Preferably said micro-organisms are bacteria. In a preferred embodiment, the assay of the present invention is characterized in that it comprises the use of at least one molecular marker that is conserved in Gram-positive bacteria and at least one molecular marker that is conserved in Gram-negative bacteria.

In the prior art, in order to detect the presence of bacteria in samples or tissues, extremely conserved molecular markers are generally used. The most commonly used sequences for detecting bacteria are the sequence of the gene coding for ribosomal DNA (16s rDNA gene) (Klaschik et al, 2002) and the 16S-23S intergenic region (Gurtler & Stanisich, 1996). However, ribosomal gene 16S rDNA does not always allow the distinction between species, as illustrated for the *Bacillus* species (La Scola et al, 2003). This is a major drawback in the 16S rDNA gene sequence identification method, because in some species, a sequence can be ambiguous since it does not distinguish between two closely related

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clinical species but disclosing however a distinct virulence phenotype (for instances, *Escherichia coli* K12 versus *Escherichia coli* O157:H7). This remark applies to the intergenic spacer 16S-23S rDNA as well (Gianinno *et al*, 2003). There is therefore a need to develop a molecular identification system which better discriminate bacteria than the 16S rDNA and the intergenic spacer 16S-23S rDNA.

In accordance with the present invention two series of conserved molecular markers were identified and characterized which are extremely suitable for permitting the detection and genotyping of micro-organisms, and in particular of bacteria, in a Gram-specific way. More in particular these molecular markers comprise on one hand markers preferentially conserved in Gram-positive bacteria and the other hand markers that are preferentially conserved in Gram-negative bacteria. The present invention now allows, by a combined use of these two types of conserved molecular marker sequences, to detect bacteria in a sample and to genotype these bacteria in a gram-specific way as well as in a genera-, species-, and even sometimes, strain-specific manner.

So far, in conventional microbiology, one distinguishes the bacteria according to the structure of their wall (the wall is present in all bacteria except mycoplasms). This structure conditions the color of bacteria after Gram staining (Gram is made of several successive steps including treatment with purple gentian, Lugol's solution, alcohol and fuchsine). The bacteria whose wall is permeable to alcohol lose their purple staining (violet gentian) and coloured in red (fuchsine), defining so what is considered as a Gram-negative bacteria. In Gram-positive bacteria, the wall is primarily made by peptidoglycane. In Gram-negative bacteria, the peptidoglycane layer is thin and the wall has a more complex structure. In the clinical practice, the choice of antibiotherapy relies primarily on Gram stain. Indeed, antibiotics targeting the bacterial wall are much more on Gram-positive bacteria. As already stated above, several clinical studies show that any delay with the initiation of antibiotherapy results in increased mortality and hospital morbidity. Practically, the microbiologic identification (culture) comes too late.

Such approach provides many advantageous compared to conventionally applied detection strategies, wherein no such gram-specificity is involved. The present invention now permits by the use two series of conserved molecular markers to rapidly determine the gramphenotype of bacteria in a sample and as a consequence to rapidly determine the most suitable antibiotherapy to be applied. This can be substituted to the conventional Gram staining procedure which is far less sensitive.

In a preferred embodiment, the assay of the present invention is further characterized in that the molecular maker that is conserved in Gram-positive bacteria comprises PurA or

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Pstl. In a more preferred embodiment the molecular maker that is conserved in Gram-positive bacteria is selected from the group comprising the Spy0160 (marker I), Spy1372 (marker II), SpyM3_0902 & SpyM3_0903 (marker III) and Spy1527 (marker IV) marker sequences. In yet another more preferred embodiment, the molecular maker that is conserved in Gram-positive bacteria is selected from the group comprising the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

Another preferred embodiment of the invention relates to an assay that is characterized in that the molecular maker that is conserved in Gram-negative bacteria is selected from the group comprising the Ecs0036 (marker V), HI1576 (marker VI), EG10839 and EG11396 (marker VII), and HI0019 (marker VIII) sequences.

In yet another preferred embodiment the molecular maker that is conserved in Gramnegative bacteria is selected from the group comprising the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

Table 1 summarizes sequences used in accordance with the present invention for the detection and identification of Gram-positive and Gram-negative bacteria.

Table 1

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		Gram	-positive bacteria		
Sequence	Gene	Marker	Sequences found in Gram- positive bacteria (SEQ ID NOs:)	Overlapping sequences found in Gram- negative bacteria (SEQ ID NOs:)	Sequences found in other organisms (SEQ ID NO:)
Spy0160	PurA		1-62 ; 326-359	63	
Spy1372	Pstl	11	64-107; 109- 111;117-129; 137; 145-148; 360-395; 397- 399	108 ; 112-116 ; 130-136 ; 138- 144 ; 396 ; 400- 403	149 (Cryptococcus neoformans)
SpyM3_0902 & SpyM3_0903	Hypothetical protein	III	150-180; 404- 412		
Spy1527	Hypothetical protein	IV	181-193; 413- 425		

Sequence Gene Marker Sequences found in Gram-negative bacteria

Sequences found in Gram-negative bacteria

Sequences found in Gram-positive bacteria

Sequences found in Gram-positive bacteria

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Ecs0036	carB	V	194-232 ; 238- 239 ; 242-254 ; 431-442	233-237 ; 240- 241 ; 255	
HI1576	pgi	VI	256-277; 426- 430		
EG10839 & EG11396	sfrB & yigC	VII	278-303; 443- 451		
HI0019	yleA	VIII	304-325; 452- 461		

The present invention also relates to the use of an assay as defined herein for diagnosing bacterial infection of a sample.

The foregoing and other objects, features and advantages of the invention will become more readily apparent from the following detailed description of preferred embodiments.

Description of the figures

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Figure 1 represents the amplification of a molecular marker I (Spy0160 or *pur A)* in Grampositive bacteria.

Figure 2 represents the amplification of a molecular marker II (Spy1372 or *ptsI*) in Grampositive bacteria.

Figure 3 represents the amplification of a molecular marker III (SpyM3_0902 & SpyM3_0903) in Gram-positive bacteria.

Figure 4 represents marker I (purA) sequences amplified from different Gram-positive bacteria (SEQ ID NOs 1-62), and from a Gram-negative bacterium (SEQ ID NO: 63)

Figure 5 represents marker II (pstI) sequences amplified from Gram-positive bacteria (SEQ ID NOs: 64-107; SEQ ID NOs: 109-111, SEQ ID NOs: 117-129, SEQ ID NO: 137, SEQ ID NOs 145-148), from some Gram-negative bacteria (SEQ ID NOs 108, 112-116, 130-136, 138-144) and from the fungi *Cryptococcus neoformans* (SEQ ID NO: 149).

Figure 6 represents marker III (SpyM_0902 &SpyM_0903) sequences amplified from Grampositive bacteria (SEQ ID NOs 150-180).

Figure 7 represents marker IV (putative GTP-binding factor plus 160 nt downstream this ORF) sequences amplified from Gram-positive bacteria (SEQ ID NOs 181-193)

Figure 8 represents the amplification of a molecular marker V (Ecs0036 or carB) in Gramnegative bacteria.

Figure 9 represents sequences amplified with molecular marker V (carB) from various Gramnegative bacteria (SEQ ID NOs 194-232, 238-239, 242-254) and from various Gram-positive bacteria (SEQ ID NOs 233-237, 240-241, 255)

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Figure 10 represents the amplification of a molecular marker VI (HI1576 or pgi) in Gramnegative bacteria.

- **Figure 11**, represents sequences amplified with molecular marker VI (HI1576 or pgi) from various Gram-negative bacteria (SEQ ID NOs 256-277).
- Figure 12 represents sequences amplified with molecular marker VII (EG10839 & EG11396 or sfrB & yigC) in Gram-negative (SEQ ID NOs 278-303).
 - **Figure 13** represents sequences amplified with molecular marker VIII (HI0019 or hypothetic yleA protein) in Gram-negative bacteria (SEQ ID NOs 304-325).
- **Figure 14** represents marker I (Spy0160 or purA) sequences amplified from different Grampositive bacteria (SEQ ID NOs 326-359).
 - **Figure 15** represents marker II (Spy1372 or pstI) sequences amplified from Gram-positive bacteria (SEQ ID NOs: 360-395; SEQ ID NOs: 397-399), and some Gram-negative bacteria (SEQ ID NOs 396, 400-403).
- **Figure 16** represents marker III (SpyM_0902 &SpyM_0903) sequences amplified from Gram-positive bacteria (SEQ ID NOs 404-412).
 - **Figure 17** represents marker IV (Spy1527, a putative GTP-binding factor plus 160 nt downstream) sequences amplified from Gram-positive bacteria (SEQ ID NOs 413-425).
 - **Figure 18** represents sequences amplified with molecular marker VI (HI1576 or pgi) from various Gram-negative bacteria (SEQ ID NOs 426-430).
- Figure 19 represents sequences amplified with molecular marker V (Ecs0036 or carB) from various Gram-negative bacteria (SEQ ID NOs 431-442).
 - **Figure 20** represents sequences amplified with molecular marker VII (EG10839 & EG11396 or sfrB & yigC) in Gram-negative (SEQ ID NOs 443-451).
- Figure 21 represents sequences amplified with molecular marker VIII (HI0019, hypothetic yleA protein) in Gram-negative bacteria (SEQ ID NOs 452-461).

Detailed description of the invention

The following definitions serve to illustrate the terms and expressions used in the different embodiments of the present invention as set out below.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. For example, with regards to genomic DNA, the term "isolated" includes nucleic acid molecules which are separated from the chromosome with which the genomic DNA is naturally associated.

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The term "probe" or "nucleic acid probe" refers to single stranded sequence-specific oligonucleotides which have a base sequence which is sufficiently complementary to hybridize to the target base sequence to be detected.

The term "primer" refers to a single stranded DNA oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer, extension product which is complementary to the nucleic acid strand to be copied. The length and the sequence of the primer must be such that they allow to prime the synthesis of the extension products. Preferably the primer is about 5-50 nucleotides long. Specific length and sequence will depend on the complexity of the required DNA or RNA targets, as well as on the conditions of primer use such as temperature and ionic strength.

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The term "target" refers to nucleic acid molecules originating from a biological sample which have a base sequence complementary to the nucleic acid probe of the invention. The target nucleic acid can be single-or double-stranded DNA (if appropriate, obtained following amplification) and contains a sequence which has at least partial complementarity with at least one probe oligonucleotide.

The phrase "a (biological) sample" refers to a specimen such as a clinical sample (pus, sputum, blood, urine, etc.) of human or animal, an environmental sample, bacterial colonies, contaminated or pure cultures, purified nucleic acid, etc. in which the target sequence of interest is sought.

The term "polynucleic acid" corresponds to either double- stranded or single-stranded cDNA or genomic DNA, containing at least 10, 20, 30, 40 or 50 contiguous nucleotides.

A polynucleic acid which is smaller than 100 nucleotides in length is often also referred to as an oligonucleotide. Single stranded polynucleic acid sequences are always represented in the present invention from the 5' end to the 3' end. By "oligonucleotide" is meant a nucleotide polymer generally about 10 to about 100 nucleotides in length, but which may be greater than 100 or shorter than 10 nucleotides in length.

The term "homologous" is synonymous for identical and means that polynucleic acids which are said to be e. g. 90% homologous show 90% identical base pairs in the same position upon alignment of the sequences.

"Hybridization" involves the annealing of a complementary sequence to the target nucleic acid (the sequence to be detected). The ability of two polymers of nucleic acid containing complementary sequences to find each other and anneal through base pairing interaction is a well-recognized phenomenon.

The term "stringency" indicates one used to describe the temperature and solvent composition existing during hybridization and the subsequent processing steps. Under high

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stringency conditions only highly complementary nucleic acid hybrids will form; hybrids without a sufficient degree of complementarity will not form. Accordingly, the stringency of the assay conditions determines the amount of complementarity needed between two nucleic acid strands forming a hybrid. Stringency is chosen to maximize the difference in stability between the hybrid formed with the target and the non-target nucleic acid.

By "complementary" is meant a property conferred by the base sequence of a single strand of DNA which may form a hybrid or double stranded DNA: DNA, through hydrogen bonding between Watson-Crick base pairs on the respective strands. Adenine (A) usually complements thymine (T), while guanine (G) usually complements cytosine (C).

By "hybrid" is meant the complex formed between two single stranded nucleic acid sequences by Watson-Crick base pairings or non-canonical base pairings between the complementary bases.

Molecular Marker sequences

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In a first aspect, the present invention provides conserved molecular markers for the detection and/or identification of one or more micro-organisms, and preferably bacteria. More in particular, the present invention provides two series of conserved molecular markers which are extremely suitable for permitting the detection and genotyping of micro-organisms, and in particular of bacteria, in a Gram-specific way.

The term "molecular marker" and "molecular marker sequence" are used herein as synonyms. These terms refer to isolated and purified nucleic acid (DNA) molecules. The term "conserved molecular marker" as used herein refers to a coding or non coding DNA sequence, which can be found in the genome of various bacterial species, showing a sequence identity with an original sequence which is superior to or equal to 50%, and preferably superior to or equal to 80%.

According to the present invention, two series of conserved genetic markers were characterized: one preferentially conserved in Gram-positive bacteria and the other preferentially conserved in Gram-negative bacteria.

In a preferred embodiment, the molecular markers that are conserved in Gram-positive bacteria comprise Spy0160 (PurA) or Spy1372 (PstI). More preferably the markers that are conserved in Gram-positive bacteria are selected from the group comprising Spy0160 Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527 marker sequences

In another preferred embodiment, the molecular markers that are conserved in Gram-positive bacteria are any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

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In yet another preferred embodiment, the molecular markers that are conserved in Gram-negative bacteria are selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396, and HI0019.

In another preferred embodiment, the molecular markers that are conserved in Gramnegative bacteria are any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461. However, it should be clear from the present invention that the present invention is not limited to the molecular marker sequences conserved in Gram-positive and in Gram-positive bacteria as described herein. Other conserved molecular marker sequences that can be characterized and identified for various other Gram- positive bacteria and other Gram-negative bacteria including according to the invention are considered to be included in the present application as well.

In another embodiment, the invention relates to the use of at least two conserved molecular markers for detecting bacteria in a sample.

In a preferred embodiment, the invention relates to the use of at least two conserved molecular markers for detecting and genotyping a bacterium on the basis of the Gram phenotype in a sample. Preferably, the invention relates to the use of at least one molecular marker that is conserved in Gram-positive bacteria and at least one molecular marker that is conserved in Gram-negative bacteria for detecting and genotyping a bacterium. In particularly preferred embodiment, the invention relates to the use of at least one molecular marker that is conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one molecular marker that is conserved in Gram-negative bacteria and that is selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396, HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

The present invention thus provides for highly conserved molecular markers that can be used for detecting the molecular presence of micro-organisms, and in particular of bacteria, in samples and/or tissues, including in cultured samples which give a false-negative result using conventional detection techniques. The present conserved markers can also advantageously be used for detecting the molecular presence of micro-organisms, and in particular of bacteria, in samples from tissues showing bacterial background. In the latter case, the conserved molecular markers are preferably used in combination with specific

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primers or probes that directly target a pre-defined panel of bacteria of interest and that exclude the "background flora". A suitable pre-defined panel of bacteria of interest may, for instance, include bacteria involved in community-acquired pneumonia, such as but is not limited to Haemophilus influenzae, Legionella species, Staphylococcus aureus, Moraxella catarrhalis, Gram-negative enteric bacteria.

It is further noted that the molecular identification of Gram phenotype is based on partially overlapping Gram-positive and Gram-negative markers. It must born in mind that, unlike in the present invention, another conserved marker (16S) shows an extensive overlap between Gram-positive and Gram-negative bacteria. In the present case, using concomitantly both series of partially overlapping markers in a combined way makes it possible to cover a much broader spectrum of bacterial pathogens while defining also precisely the Gram phenotype of those pathogens. The strategy relies upon the molecular detection of gene preferentially present in Gram-positive or Gram-negative bacterial. Each series of markers allows therefore improving overall detection in their respective group (either Gram-positive bacteria for preferentially Gram-positive markers, or Gram-negative bacteria for preferentially Gram-negative markers). Considering the somehow overlapping specificity for both groups, (overlap within the Gram-positive specificity for Gram-negative markers and overlap within the Gram-positive specificity for Gram-negative markers), the power of the molecular discrimination is even increased for some bacteria targeted by both groups of markers. This combined strategy overcomes the potential lack of specificity obtained when using one single marker towards some species, as is for instance the case when using a 16S marker.

In addition, the use of different markers which are mapped on different loci in the bacteria also improves the quality of the diagnosis in that it can more easily circumvent false positive reactions due to accidental PCR contamination hampering the use of one particular marker.

Primers and probes derived from conserved molecular markers

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In another embodiment, the invention relates to a primer pair (forward and reverse primers) suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria. More preferably, the invention relates to a primer pair suitable for amplifying any of the conserved molecular marker sequences that are conserved in Gram-positive bacteria as defined herein, and that are preferably selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID

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NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

In another embodiment, the invention relates to a primer pair (forward and reverse primers) suitable for amplifying a molecular marker that is conserved in Gram-negative bacteria. More preferably, the invention relates to a primer pair suitable for amplifying any of the conserved molecular marker sequences that are conserved in Gram-negative bacteria as defined herein, and that are preferably selected from the group comprising Ecs0036, HI1576,, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

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The primers of the present invention include at least 15-mer oligonucleotide and are preferably 70%, 80%, 90% or more than 95% homologous to the exact complement of the target sequence to be amplified. Those primers are about 15 to 50 nucleotides long, and preferably about 15 to 35 nucleotides long. Of course, primers consisting of more than 50 nucleotides can be used.

The present invention also relates to a nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria. More preferably, the invention relates to a nucleic acid probe capable of hybridizing any of the molecular marker sequences that are conserved in Gram-positive bacteria as defined herein, and that are preferably selected from the group comprising Spy0160 (PurA), Spy1372 (PstI), SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

In another embodiment, the present invention also relates to a nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria. More preferably, the invention relates to a nucleic acid probe capable of hybridizing any of the molecular marker sequences that are conserved in Gram-negative bacteria as defined herein, and that are preferably selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

The probe of the present invention preferably includes at least 15-mer oligonucleotide and are preferably 70%, 80%, 90% or more than 95% homologous to the exact complement of the target sequence to be detected. Those probes are preferably about 15 to 50 nucleotides long. The primers and probes of the invention can be used, for diagnostic purposes, in investigating the presence or the absence of a target nucleic acid in a biological

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sample, according to all the known hybridization techniques such as for instance dot blot, slot blot, hybridization on arrays including nanotools, real-time PCR, etc...

The probes of the invention will preferably hybridize specifically to one or more of the above-mentioned molecular marker sequences.

The primers of the invention may amplify specifically one or more of the above-mentioned marker sequences. The design of specifically hybridising probes is within the skilled person's knowledge. Also the design of primers which can specifically amplify certain sequences or molecular markers is within the skilled person's knowledge.

The nucleic acid probes of this invention can be included in a composition or kit which can be used to rapidly determine the presence or absence of pathogenic species of interest (see below).

Compositions

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In another embodiment, the invention relates to a composition. In a preferred embodiment, the invention relates to a composition comprising at least one primer pair (forward and reverse primers) suitable for amplifying a conserved molecular marker that is conserved in Gram-positive bacteria and at least one primer pair (forward and reverse primers) suitable for amplifying a conserved molecular marker that is conserved in Gram-negative bacteria.

Preferably, the composition comprises at least one primer pair suitable for amplifying any of the molecular marker sequences that are conserved in Gram-positive bacteria and that are selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one primer pair suitable for amplifying any of the molecular marker sequences that are conserved in Gram-negative bacteria and that are selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

In yet another embodiment, the invention relates to a composition comprising at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria. Preferably, the composition comprises at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372,

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SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

By "composition", it is meant that primers or probes complementary to bacterial DNA may be in a pure state or in combination with other primers or probes. In addition, the primers or probes may be in combination with salts or buffers, and may be in a dried state, in an alcohol solution as a precipitate, or in an aqueous solution.

Kits

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In yet another embodiment, the invention relates to a kit for detecting and identifying one or more micro-organisms, preferably bacteria, in a sample, which comprises:

- a) a composition comprising at least one primer pair (forward and reverse primers) suitable for amplifying a conserved molecular marker that is conserved in Gram-positive bacteria and at least one primer pair (forward and reverse primers) suitable for amplifying a conserved molecular marker that is conserved in Gram-negative bacteria; for amplifying polynucleic acids in said sample,
- b) a composition comprising at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria,
- c) a buffer enabling hybridization reaction between the probes contained in said composition and the polynucleic acids present in said sample or amplified products therefrom or components necessary for producing the buffer,
- d) a solution for washing hybrids formed under the appropriate wash conditions or components necessary for producing the solution, and
 - e) optionally a means for detection of said hybrids.

A kit according to the invention preferably includes all components necessary to assay for the presence of bacteria. In the universal concept, the kit includes a stable preparation of labeled probes, hybridization solution in either dry or liquid form for the hybridization of target and probe polynucleotides, as well as a solution for washing and

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removing undesireable and nonduplexed polynucleotides, a substrate for detecting the labeled duplex, and optionally an instrument for the detection of the label.

In a preferred embodiment, the present kit comprises a composition which comprises at least one primer pair suitable for amplifying any of the molecular marker sequences that are conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one primer pair suitable for amplifying any of the molecular marker sequences that are conserved in Gram-negative bacteria selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

In yet another preferred embodiment, the present kit comprises a composition which comprises at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one at least one nucleic acid probe capable of hybridising to a molecular marker that is conserved in Gram-negative bacteria selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

In yet another preferred embodiment, the kit according to the present invention further comprises one or more genus-, species and/or strain-specific nucleic acid probes capable of hybridizing to a genus-, species and/or strain-specific bacterial polynucleotide sequence.

DNA chip

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In another preferred embodiment, the present invention provides a DNA chip in which nucleic acid probes are immobilized on a solid support. The invention relates to the manufacturing of a solid support (array –DNA chip) on which several sets of nucleic acid probes are covalently bound or directly synthesized.

In a preferred embodiment, the invention relates to a DNA chip in which at least one of nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Grampositive bacteria, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria, is immobilized on a solid support.

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Preferably, the DNA chip comprises at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461 immobilized on a solid support.

In yet another preferred embodiment, the DNA chip according to the present invention further comprises one or more genus-, species and/or strain-specific nucleic acid probes capable of hybridizing to a genus-, species and/or strain-specific bacterial polynucleotide sequence.

The DNA chip which is formed by arranging DNA fragments of variety of base sequences on the surface of a narrow substrate in high density is used in finding out the information on DNA of an unknown sample by hybridization between an immobilized DNA and unknown DNA sample complementary thereto. Examples of the solid carrier on which the probe oligonucleotides are fixed include inorganic materials such as glass and silicon and polymeric materials such as acryl, polyethylene terephtalate (PET), polystyrene, polycarbonate and polypropylene. The surface of the solid substrate can be flat or have a multiple of hole. The probes are immobilized on the substrate by covalent bond of either 3'end or 5'end. The immobilization can be achieved by conventional techniques, for example, using electrostatic force, binding between aldehyde coated slide and amine group attached on synthetic oligomeric phase or spotting on amine coated slide, L- lysine coated slide or nitrocellulose coated slide. The immobilization and the arrangement of various probes onto the solid substrate are carried out by pin microarray, inkjet, photolithography, electric array, etc.

The term "DNA chip" as used herein, is to be understood in its broadest sense, i.e. including nanochips or nanotools that are designed to recognize a specific pattern of nucleic acids through hybridization.

Assay

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In another embodiment, the invention relates to an assay for detecting and identifying one or more micro-organisms, preferably bacteria, in a sample, characterized in that said assay comprises the use of at least two conserved molecular markers, and preferably

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comprises the use of at least one molecular marker that is conserved in Gram-positive bacteria and at least one molecular marker that is conserved in Gram-negative bacteria.

In the prior art, ultimate molecular species identification results classically from sequence analysis of an amplification product and the comparison of this sequence with those which are available in public DNA database (for instance, GeneBank...). The sequence analysis requires nearly 24 hours to complete the various analytical steps: amplicon purification, cycle sequencing, reading and interpretation of the results.

The present invention provides a strategy which permits to significantly reduce the time requested for genera, species, and optionally strain, identification of bacteria in a sample compared to classical identification strategies as described above. More in particular, the present strategy preferably consists in amplifying a set of conserved genetic markers and either to hybridize produced amplicons on specific capture probes covalently bound on an array or, alternatively, to hybridize a specific probe during the amplification step (e.g. real-time PCR with Taqman or molecular Beacon probes). The result of the identification will include information regarding the Gram phenotype of bacteria present in the sample of interest (or a combination of both Gram phenotype in case of mixed infections with Gram-positive and Gram-negative), as well as information on genera and species to which they belong. The final results will integrate all the hybridization signals generated by the selected markers.

In a preferred embodiment, the method for detecting and identifying one or more micro-organisms, preferably bacteria, in a sample may comprise the following steps:

- a) If appropriate isolating and/or concentrating the DNA present in said sample;
- b) amplifying said DNA with

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- at least one pair of (forward and reverse) primers suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria, and
- at least one pair of (forward and reverse) primers suitable for amplifying a molecular marker that is conserved in Gram-negative bacteria.
- c) hybridizing the amplified DNA fragments obtained in step b) with genus-, and/or species-, and/or strain-specific primers or nucleic acid probes
- d) detecting the hybrids formed in step c) and
- e) identifying micro-organisms in said sample from the differential hybridization signals obtained in step d)

The present invention allows to detect the presence of bacteria in human, animal and/or environmental samples, and, at the same time, to identify those bacteria, including, highly pathogenic ones. Such detection and identification system is based on the pattern of

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hybridization of several combined DNA fragments. Identification relies upon concomitant signals generated by a panel of unrelated markers. The system provides discrimination based on the Gram-phenotype as well as genus- and species-specificity.

To provide nucleic acid substrates for use in the detection and identification of microorganisms in clinical samples using the present assay, nucleic acid, preferably DNA, is extracted from the sample. The nucleic acid may be extracted from a variety of clinical samples, or environmental samples, using a variety of standard techniques or commercially available kits.

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A second step is an amplification of the desired DNA region of the target DNA by PCR. Examples of the PCR include most typical PCR using the same amounts of forward and reverse primers, multiplex PCR in which a multiple of target DNAs can be amplified at once by adding various primers simultaneously, ligase chain reaction (LCR) in which target DNA is amplified using specific 4 primers and ligase and the amount of fluorescence is measured by ELISA (Enzyme Linked Immunosorbent Assay), and the other PCR such as Hot Start PCR, Nest-PCR, DOP-PCR (degenerate oligonucleotide primer PCR), RT-PCR (reverse transcription PCR), Semi-quantitative RT-PCR, Real time PCR, RACE (rapid amplification of cDNA ends), Competitive PCR, STR (short tandem repeats), SSCP (single strand conformation polymorphism), DDRT-PCR (differential display reverse transcriptase), etc.

A further step comprises the hybridization of the amplified DNA fragments obtained in step b) with specific primers or nucleic acid probes. The choice of the applied hybridization technique should not be considered as limitative for the present invention. Nanotools can also be designed to recognize a specific nucleic acid pattern with or without PCR amplification.

In one embodiment, step c) may include an identification by contacting the amplified DNA fragments obtained in step b) with a composition comprising at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria. In such case, steps b) and c) of the above described method are performed subsequently. For instance, identification may be performed using a reverse hybridization procedure (dot blot, slot blot, hybridization on micro-, macro- or nano-arrays, etc....) In such case, hybridization of marked amplicons is performed on Gram-, genera- and species-specific nucleic acid probes bound covalently on the array (e.g. micro- or macro-arrays). While the result is visual, the reading can also be automated, facilitating therefore the use in the clinical practice.

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In another embodiment, step c) may include the use of real-time PCR with specific probes (multiplex approach) which allows to have a specific result in a couple of hours. Simplex or multiplex PCR techniques in real-time include the use of specific acid probes on a DNA target during the PCR step (e.g. Taqman probes, molecular beacons or MGB (Minor Groove Binding) probes, etc...). In such case, steps b) and c) of the above described method are performed simultaneously. A significant advantage of using a real-time PCR technique is the increased speed, e.g. only a couple of hours are required for obtained final results. This is mainly due to the reduced cycle times, removal of separate post-PCR detection procedures, and the use of sensitive fluorescence detection equipment, allowing earlier amplicon detection. Another advantage of a real-time PCR technique is that it is a single tube procedure with the reading during the PCR and no manipulation required at the end of the procedure. This single tube procedure prevents therefore the risk of molecular contamination existing with other PCR procedures, including micro- and macro-array techniques. Preferably a nested real-time PCR strategy is used to increase the sensitivity of the method with a detection limit of one DNA copy in tissue samples.

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The formed hybrids can be quantified by labeling the target with a fluorescence or radioactive isotope in accordance to conventional methods. The labeling may be carried out by the use of labeled primers or the use of labeled nucleotides incorporated during the polymerase step of the amplification.

According to a preferred embodiment of the present invention, the primers suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria used in step b) of the above mentioned method preferably comprise primers suitable for amplifying a molecular marker selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

According to another preferred embodiment of the present invention, the primers suitable for amplifying a molecular marker that is conserved in Gram-negative bacteria used in step b) of the above mentioned method preferably comprise primers suitable for amplifying a molecular marker selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

The following examples are meant to illustrate the present invention. **Examples 1-3** present and describe molecular marker sequences that have been characterized on a wide panel of clinical and reference bacterial genera species and bacterial strains and that allow the discrimination between Gram-positive and Gram-negative bacteria as well as genera and

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species identification. **Example 4** illustrates the use of molecular markers according to the present invention for the detection and identification of Bacillus bacteria and for the discrimination between various Bacillus strains of the same species. **Example 5** illustrates nucleic acid probes according to the present invention.

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Examples

Example 1 Characterization of molecular markers of genes enabling the identification of Gram-positive bacteria

The present example aims to test the Gram-positive specificity of several markers. The list of Gram-positive bacteria used in the present example (study of markers specificity) is given in table 2A.

 Table 2A
 Gram-positive bacteria

genus	species	strain reference
Bacillus	anthracis	1978
Bacillus	anthracis	STERNE
Bacillus	anthracis	BUTARE
Bacillus	anthracis	1655H85
Bacillus	anthracis	CODA - CERVA
Bacillus	anthracis	2054H82
Bacillus	cereus	ATCC10987
Bacillus	cereus	ATCC 14579
Bacillus	pumilus	Clinical
Bacillus	species	Clinical
Bacillus	thuringiensis kurstaki	T03A016 HD_1
Bacillus	thuringiensis israelensis	4Q2_72
Bacillus	mycoides	MYC003
Bacillus	mycoides	NRS306
Bacillus	weihenstephanensis	WSBC10204
Bacillus	halodurans	DSMZ 497
Bacillus	firmus	DSMZ 12643
Bacillus	megatherium	DSMZ 1324
Bacillus	pseudomycoïdes	DSMZ 12442
Clostridium	difficile	DSMZ 1296
Clostridium	perfingens	DSMZ 756
Enterococcus	faecium	DSMZ 6177
Enterococcus	faecalis	DSMZ 2570
Enterococcus	flavescens	DSMZ 7370
Enterococcus	durans	DSMZ 20633
Enterococcus	casseliflavus	DSMZ 20680
Enterococcus	gallinarum	DSMZ 20628
Enterococcus	hirae	DSMZ 20160
Enterococcus	raffinosus	DSMZ 75633

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EnterococcusaviumDSMZ 2067EnterococcusvillorumCODA - CERLactococcuslactisDSMZ 2048ListeriamonocytogenesDSMZ 2060	VA 1
LactococcuslactisDSMZ 2048ListeriamonocytogenesDSMZ 2060	1
	0
Listeria innocua DSMZ 2064	
Staphylococcus aureus ATCC 3588	4
Staphylococcus epidermidis ATCC 1499	0
Staphylococcus hominis ATCC 2784	4
Staphylococcus haemolyticus ATCC 2997	0
Staphylococcus saprophyticus ATCC 1530	
Staphylococcus xylosus ATCC 3566	
Staphylococcus simulans ATCC 2784	
Staphylococcus cohnii cohnii ATCC 3566	
Staphylococcus capitis capitis ATCC 2784	
Staphylococcus sciuri ATCC 2906	
Staphylococcus warneri ATCC 2783	
Staphylococcus lugdunensis ATCC 4380	
Staphylococcus gallinarum ATCC C357	
Staphylococcus schleiferi schleiferi ATCC 4380	
Staphylococcus capitis ureolyticus ATCC 4932	
Staphylococcus cohnii urealyticum ATCC 4933	
Staphylococcus auricularis ATCC 3375	
Staphylococcus caseolyticus ATCC 1354	
Staphylococcus intermedius ATCC 2966	
Streptococcus pyogenes DSMZ 2056	
Streptococcus agalactiae DSMZ 2134	
Streptococcus pneumoniae DSMZ 2056	1
Streptococcus oralis DSMZ 2062	
Streptococcus sanguinis DSMZ 2056	
Streptococcus mitis DSMZ 1264	
Streptococcus gordonii DSMZ 6777	
Streptococcus canis DSMZ 2038	
Streptococcus mutans DSMZ 2052	3
Streptococcus subspecies Clinical	
Streptococcus bovis DSMZ 2048	
Streptococcus thermophilus DSMZ 2061	
Streptococcus suis DSMZ 9682	2

The following sequences have been characterized and used for multigenotypic identification of Gram-positive bacteria.

The **Spy0160 sequence** (marker I) from *Streptococcus pyogenes* (accession number: AE006485.1; position 3201 to 4030) is part of an open reading frame homologous for the gene purA. The purA protein plays an important role in the *novo* bacterial synthesis of purines. It catalyses the synthesis of adenylosuccinate starting from inosine monophosphate (IMP) and of aspartate, and using energy provided by the GTP. The first nucleotides alignments performed suggested the existence of conserved sequences similar to the

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Spy0160 sequence in a few Gram-positive bacteria. These findings have been extended to a wide panel of bacteria that were available in our DNA bank and confirmed that this marker was present in almost all Gram-positive bacteria and was very helpful in discrimination of closely related Gram-positive species and in many cases could allow discrimination between strains of the same species

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A second marker is the **Spy1372 sequence** (Marker II) from *Streptococcus pyogenes* (accession n° AE004092, position 1139277 to 1141010). The corresponding gene probably encodes an enzyme involved in the transport of sugar in bacteria. Indeed, this gene is homologous to gene ptsI of *Staphylococcus aureus* coding for a phosphoenol pyruvate phosphatase (accession n° NC_002758, from position 1137273 to 1138991). This gene is part of PTS operon (phosphotransferase system) including several genes coding for proteins involved in importation of sugar by bacteria (Plumbridge *et al*, 2002). The product of ptsI gene is a protein called Enzyme I, which may be phosphorylated by phosphoenol pyruvate. Phosphorylated Enzyme I can give its phosphate group to another protein of the PTS group through a cascade which leads to the entry of glucose in the bacterial periplasm (Stentz *et al*, 1997).

A third marker is the **SpyM3_0902 - SpyM3_0903 sequence** (Marker III) from *Streptococcus pyogenes* MGAS315 (accession n° AE014154, from position 40670 to 41160). This sequence is located downstream the gene encoding alpha-helicase and corresponds to the open reading frame of a hypothetical protein.

A fourth marker is the **Spy1527 sequence** (Marker IV) from *Streptococcus pyogenes* from position 1201 to 2464, including nucleotides 2465 to 2625 (accession n° AE006586). The Spy1527 sequence corresponds to the gene *typA*, coding for a putative GTP-binding protein (GTP-BP). The fragment from position 2465 to 2625 does not correspond to an open reading frame, but is a non-coding sequence.

A first analysis of some available complete bacterial genomes suggests that homologous sequences were present in most of those bacteria.

A further analysis has been performed on reference strains and on several hundreds clinical strains provided by Belgian hospitals. The conservation of targets of interest (purA and ptsI (i.e. Marker I and II) has been confirmed in the genome of all these reference and clinical strains. This analysis confirmed the very little genomic variability of these sequences within a species of interest. This feature is crucial to allow the use of these marker sequences in a strategy of multigenotypic identification of Gram-positive bacteria.

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Example 2 Characterization of molecular markers of genes enabling the identification of Gram-negative bacteria

The present example aims to test the Gram-negative specificity of several markers. The list of Gram-positive bacteria used in the present example (study of markers specificity) is given in **table 2B**.

Table 2B Gram-negative bacteria

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genus	species	strain reference
Acinetobacter		ATCC 19606
Acinetobacter	calcoaceticus	DSMZ 1139D
Bordetella	parapertussis	Clinical
Bordetella	bronchiseptica	Clinical
Bordetella	pertusis	Clinical
Brucella	melitensis biovar 1	16M
Brucella	melitensis biovar 2	63/9
Brucella	abortus biovar 1	544
Brucella	abortus biovar 2	86/8/59
Brucella	canis	RM6/66
Brucella	ovis	63/290
Brucella	suis biovar 1	1330
Brucella	suis biovar 2	686
Burkholderia	cepacia	ATCC 17770
Citrobacter	freundii	DSMZ 30039
Cryptococcus	neoformans	DSMZ 70219
Enterobacter	cloaceae	ATCC 13047
Enterobacter	aerogenes	DSMZ 13048
Escherishia	coli O157:H7	DSMZ 8579
Escherishia	coli K12	DSMZ 6367
Francisella	tularensis	SVA / T7
Haemophilus	influenzae	DSMZ 9999
Haemophilus	ducrei	-
Klebsiella	pneumoniae	ATCC 13883
Klebsiella	oxytica	ATCC 43863
Legionella	pneumophilia	DSMZ 7513
Moraxella	catarrhalis	DSMZ 11994
Morganella	morganii	ATCC 25830
Neisseria	meningitidis groupe C	ISP ???
Neisseria	meningitidis groupe B	clinical
Pasteurella	multocida	-
Proteus	mirabilis	ATCC 29906
Proteus	vulgaris	ATCC 13315
Providencia	stuartii	ATCC 29914
Pseudomonas	aeruginosa	DSMZ 50071

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Pseudomonas	putida	ATCC 12633
Pseudomonas	syringae	ATCC 39254
Salmonella	enteritidis	Clinical
Salmonella	enterica hadar	Clinical
Salmonella	enterica brandenburg	Clinical
Salmonella	enterica derby	Clinical
Salmonella	enterica virchow	Clinical
Salmonella	enterica typhimurium	Clinical
Salmonella	enterica paratyphi B	Clinical
Serratia	liquefasciens	ATCC 27592
Serratia	marcescens	ATCC 13880
Shigella	sonnei	Clinical
Shigella	flexneri	-
Vibrio	parahaemolyticus	-
Vibrio	cholerae	-
Yersinia	pestis	-

The following sequences have been characterized and used for multigenotypic identification of Gram-negative bacteria.

The **HI1576 sequence** (marker VI) from *Haemophilus influenzae* corresponds to the gene coding for phosphoglucose isomerase (accession n° U32831, from position 12660 to 13991) an enzyme playing a role in glucidic metabolism especially for glycolysis (Morris *et al*, 2001).

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Another sequence is the **Ecs0036 sequence** (marker V) from *Escherichia coli* O157:H7 (accession n° AP002550; from position 35200 to 36200). It is believed that this sequence encodes the large carbamoyl-synthetase unit, an enzyme which catalysis the synthesis of carbamoyl phosphate, from glutamine, bicarbonate and two ATP molecules through a mechanism which requires several successive steps (Raushel *et al*, 2001). The synthesized carbamoyl-phosphate contributes to *de novo* synthesis of pyrimidic bases in bacteria (Minic *et al*, 2001).

Another sequence is the **EG10839 & EG11396 (sfrB & yigC) sequence** (= marker VII) from *Escherichia coli* K12 (accession n° NC_000913; from position 4022578 to 4024071). The corresponding protein is not yet known. When considering the sequence of the gene, it is a putative flavoprotein reductase. A search in DNA databases allowed us to find homologous sequences in some bacteria.

The **HI0019** (= marker VIII) sequence from *Haemophilus influenzae* (accession n° U32687, from position 7501 to 8550). This sequence shares all the characteristics of a coding sequence. However, the product of this coding sequence does not match any known

protein. This sequence is homologous to the gene coding for the hypothetical protein yleA from *Pasteurella multocida* (accession n° AF23940) whose function is totally unknown.

Example 3 Additional molecular marker sequences

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This example illustrates the determination of marker sequences homologous to the sequences Spy0160, Spy1372, SpyM3-0902 & SpyM3-0903, Spy1527, Ecs0036, HI1576, and EG10839 & EG11396 as defined above in other Gram-positive or Gram-negative bacteria. These marker sequences were obtained using sets of degenerated primers, which have been identified based on theoretical alignments of the above-defined marker sequence (see examples 1-2) with sequences available in DNA databases.

Table 3A-H represents some degenerated primer sequences that have been used to amplify homologous marker sequences present in other Gram-positive or Gram-negative bacteria. PCR amplification was done using the identified degenerated primers on bacterial DNA isolated from various other Gram-positive or Gram-negative bacteria. Amplification was done under conditions of low stringency. In **table 3A-H**, the conditions the PCR programs and applied temperatures are indicated.

Table 3A Target sequence: Homologs of Spy0160 (purA gene or Marker I) in Grampositive bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GRP1-S	5'-YTHTTYGAAGGDGCDCAAGG-3' (SEQ ID NO: 462)	61°C	50°C	585 bp
GRP1-AS	5'-GRYCWGGMCCWACTGAGAA-3' (SEQ ID NO: 463)	59°C	30 0	000 Бр

Table 3B Target sequence: Homologs of Spy1372 (pstl gene or Marker II) in Grampositive bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GRP2-S	5'-CCNGCCATYTCWCCRCACAT-3' (SEQ ID NO: 464)	63°C	50°C	443 bp
GRP2-AS	5'-AMGARATGAAYCCRTTCYTDGG-3' (SEQ ID NO: 465)	64°C	30 0	770 OP

Table 3C Target sequence: Homologs of SpyM3_0902 & SpyM3_0903 (Marker III) in Gram-positive bacteria

Primers	Sequence	Tm	Annealing	Amplicon
	·		temperature	size

			during the PCR	
GRP3-S	5'-GACGGAMYTCTGGAGAGACC-3'	57°C		
	(SEQ ID NO: 466)		48°C	around
GRP3-AS	5'- GCRTAYTTDGTDGCCATWCCAAA-3'	59°C	40 C	600 bp
	(SEQ ID NO: 467)		_	

Table 3D Target sequence: Homologs of Spy1527 (typA gene-Marker IV) in Grampositive bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GRP4-S	5'-GARCGTATYATGAAAATGGT-3' (SEQ ID NO: 468)	57°C	45°C	995 bp
GRP4-AS	5'-CATDCCYTCAGDCKCAT-3' (SEQ ID NO: 469)	59°C	45 C	885 bp

5 **Table 3E** Target sequence: Homologs of HI1576 (glucose-6-phosphate isomerase gene - marker VI) in Gram-negative bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GN-1-S	5'- TGGGTYGGYGGYCGTTACT-3' (SEQ ID NO: 470)	63°C	50°C	around
GN-1-AS	5'- TCGGTYTGNGCRAAGAAGTT-3' (SEQ ID NO: 471)	64°C	30 0	500 bp

Table 3F Target sequence: Homologs of Ecs0036 (Carb-P, large subunit gene- or Marker V) in Gram-negative bacteria

Primers	Sequence	Tm	Annealing	Amplicon
		,	temperature during the PCR	size
GN-2-S	5'-CSACNATYATGACYGAYCC-3' (SEQ ID NO: 472)	63°C	50°C	500-650 bp
GN-2-AS	5'-TCCATYTCRTAYTCYTTCCA-3' (SEQ ID NO: 473)	64°C	30 C	300-030 bp

Table 3G Target sequence: Homologs of EG10839 & EG11396 (sfrB & yigC or Marker VII) in Gram-negative bacteria

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Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GN-3-S	5'- AAYTTGGTRTACATRAACTG -3' (SEQ ID NO: 474)	63°C	50°C	Around 600 bp
GN-3-AS	5'- RVTGATYATGCGYTGGCT-3' (SEQ ID NO: 475)	64°C	30 C	

Table 3H Target sequence: Homologs of HI0019 (yleA or Marker VIII) in Gram-negative bacteria

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Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GN-4-S	5'- GCCNGGRAADCCNACRAT -3' (SEQ ID NO: 476)	63°C	60°C	Around 500 bp
GN-4-AS	5'- GTNTCNRTNATGGAAGGCTG-3' (SEQ ID NO: 477)	64°C	00 0	

An example of a PCR amplification used to obtain marker sequences from bacteria is as follows: 10 ng of genomic DNA from each bacterial strain tested is added to a mixture containing 10 mM Tris HCl pH 9, 2.5 mM MgCl2, 50 mM KCl, 0.1% Triton X-100 (v/v), 300 nM of each primer (forward and reverse; see **table 3** for primers used), 0.25 mM desoxynucleotides triphosphates (Roche Diagnostics, Mannheim, Germany), 2.5 U de Taq Polymerase Expand High Fidelity (Roche Diagnostics, Mannheim, Germany) in a final volume of 50 µl. Amplifications were carried out in a Mastercycler gradient (Applied Biosystem 2400, USA). An initial activation step of Expand High Fidelity (94°C for 3 min) is followed by 35 cycles (94°C for 40 s, annealing temperature equal to Tm -5 or -10 °C for 50 s, 72°C for 1 min) and a final extension for 10 min.

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Amplified DNA fragments were run on a 2% agarose gel stained with ethidiumbromide and visualized on a UV transilluminator.

Figures 1-3 illustrate the amplification in some Gram-positive bacteria of molecular markers which are homologous to markers I to III respectively. Figures 8 and 10 illustrate the amplification in some Gram-negative bacteria of molecular markers homologous to markers V (Ecs0036) and VI (HI1576) respectively. Figures 4-7, 9 and 11-21 illustrate molecular marker sequences from different Gram-positive bacteria or Gram-negative bacteria.

Example 4 Use of an assay according to the invention for molecular identification of various Bacillus species and strains

The present example illustrates the use of an assay according to the invention for the molecular identification of various *Bacillus* species, including *Bacillus anthracis*, species that cannot be discriminated with ribosomal 16S rDNA gene (La Scola *et al*, 2003). **Table 4** summarizes the results obtained for the various *Bacillus* species with the current genotyping assay. The analyses were performed using the markers I, II and III. Marker I corresponds to the Spy0160 sequence, Marker II corresponds to the Spy1372 sequence, Makrer III corresponds to the SpyM3_0902 & Spy M3_0903 sequence.

Primers where designed for these markers and with these primers DNA of *Bacillus* was amplified. Then, the obtained amplified sequences were sequenced and compared by alignment. **Table 4** indicates the number of modified nucleotides in the amplified marker sequences of these different *Bacillus* species and strains. The 16S ribosomal marker is not relevant in this context and cannot be used for identifying *Bacillus* species because the amplicons corresponding to each *Bacillus* species will give comparable nucleic acid sequences, with variations not exceeding 1% on the whole gene.

 Table 4
 Use of different molecular markers for the identification of Bacillus species

	Molecular marker	B. cereus 10987	B. cereus 14579	B. thuringiensis 4Q2-72 israelensis	B. anthracis 1978
	Marker III (SEQ ID NO: 168)		8	29	29
B. cereus 10987	Marker I (SEQ ID NO: 18)		1	23	21
	Marker II (SEQ ID NO: 70)		2	3	11
	16S		0	0	ND
	Marker III (SEQ ID NO: 169)	8		32	31
B. cereus 14579	Marker I (SEQ ID NO: 19)	1		22	20
	Marker II (SEQ ID NO: 71)	2		5	13
	16S	0		0	ND
	Marker III (SEQ ID NO: 170)	29	32		12
B. thuringiensis 4Q2-72	Marker I (SEQ ID NO: 33)	23	22		30
israelensis	Marker II (SEQ ID NO: 80)	3	5		12
	16S	0	0		ND
	Marker III (SEQ ID NO: 162)	29	31	12	
B. anthracis 1978	Marker I (SEQ ID NO: 12)	21	20	30	
	Marker II (SEQ ID NO: 64)	11	13	12	
ND - not data main	16S	ND	ND	ND	

ND = not determined

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This example shows unambiguously that the combined use of several unrelated molecular markers markedly improves bacterial species identification, as well as, to some extent, characterization of a well-determined strain within a particular species. The present

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method is so specific that it can go beyond the species identification and discriminate strains of the same species.

Example 5 Nucleic acid probes according to the present invention

This example illustrates an oligonucleotide (nucleic acid probe) that has been designed from marker I of *Staphylococcus aureus* (SEQ ID NO: 23) 5'-gtgtaggtcctacattcgtttc-3' (SEQ ID NO: 478). This oligonucleotide is specific for *S. aureus* species and can therefore allow discrimination of this species with other bacteria whereas another nucleic acid probe, the oligonucleotide 5'-cattcgtttcaaaggtaatg-3' (SEQ ID NO:479) which is located on the same marker allows discrimination of different strains of *S. aureus* (i.e. strains MRSA MW2 and MRSA COL versus strains Mu-50 and N315). These multi-resistant strains carry different methicillin resistance cassette chromosome and their resistance patterns to antimicrobials agents are different.

The illustrated nucleic acid probes can for instance advantageously be used in an assay according to the present invention, on a DNA chip according to the present invention. The two oligonucleotides provided above can be considered as specific probes which can be bound on a biochip and therefore allow discrimination between various amplicons obtained from MRSA strains amplified with the primers of **table 3**.

20 Conclusion

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The present invention demonstrates that multigenotypic molecular analyses according to Gram-, genus— species- and strain-specificity can be achieved by using concomitantly or sequentially a panel of distinct conserved molecular markers, either by conventional polymerase chain reaction PCR (with exploitation of single nucleotide specific polymorphism or SNP), real-time PCR (with/without specific Taqman probes), or post-PCR reverse hybridization on solid support (micro-, macro- or nano-array). The analyses allow a fast and specific detection of bacterial DNA and a wide bacterial genotyping in human, animal or environmental samples.

The combined use of the herein described molecular markers allows rapid and specific molecular identification of a wide panel of bacteria in samples and/or tissues, even in samples showing a background bacterial flora. To the applicant's knowledge, there is no such diagnostic tool that is based on the use of a panel of various highly conserved bacterial moleculer markers for detecting and identifying bacteria according to Gram-, genus-, species-, and to some extent also strain- classification. Compared to the existing typing systems, we believe that this is a major improvement, in view of the increased need for rapid

and multigenotypic bacterial diagnoses, especially when considering nosocomial infections and epidemic bacterial diseases occurring in a natural, accidental or criminal setting. To this respect, molecular typing of bacteria according to the Gram phenotype is of particular interest when appropriate antibiotherapy has to be rapidly started.

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PCT/EP2005/002927

Claims

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WO 2005/090596

 An assay for detecting and identifying one or more micro-organisms in a sample, characterized in that said assay comprises the use of at least two conserved molecular markers.

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- 2. Assay according to claim 1, characterized in that said micro-organisms are bacteria.
- 3. Assay according to claims 1 or 2, characterized in that said assay comprises the use of at least one molecular marker that is conserved in Gram-positive bacteria and at least one molecular marker that is conserved in Gram-negative bacteria.
 - 4. Assay according to any of claims 1 to 3, characterized in that said molecular maker that is conserved in Gram-positive bacteria is selected from the group comprising the Spy0160, Spy1372, SpyM3_0902 and SpyM3_0903, and Spy1527 sequences.
 - 5. Assay according to any of claims 1 to 3, characterized in that said molecular maker that is conserved in Gram-positive bacteria is selected from the group comprising the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.
 - 6. Assay according to any of claims 1 to 3, characterized in that said molecular maker that is conserved in Gram-negative bacteria is selected from the group comprising the Ecs0036, HI1576, EG10839 and EG11396, and HI0019 sequences.

7. Assay according to any of claims 1 to 3, characterized in that said molecular maker that is conserved in Gram-negative bacteria is selected from the group comprising the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

- 8. Use of an assay according to any of claims 1 to 7 for diagnosing bacterial infection of a sample.
- 9. A primer pair suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5.

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- 10. A primer pair suitable for amplifying a molecular marker that is conserved in Gramnegative bacteria as defined in any of claims 6 or 7.
- 5 11. A nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5.

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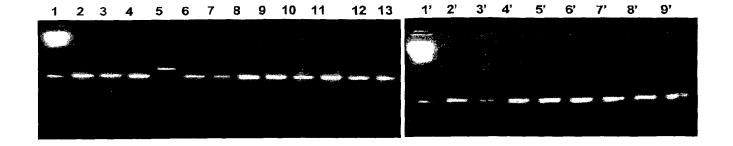
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- 12. A nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria as defined in claims 6 or 7.
- 13. A composition comprising at least one primer pair suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5, and at least one primer pair suitable for amplifying a molecular marker that is conserved in Gram-negative bacteria as defined in claims 6 or 7.
- 14. A composition comprising at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5 and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria as defined in claims 6 or 7.
- 15. A kit for detecting and identifying one or more micro-organisms, preferably bacteria, in a sample, which comprises a composition according to claim 13 and/or claim 14.
- 16. A DNA chip in which at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria as defined in claims 6 or 7, is immobilized on a solid support.

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Figure 1 Amplification of molecular marker I (pur A) in Gram-positive hacteria

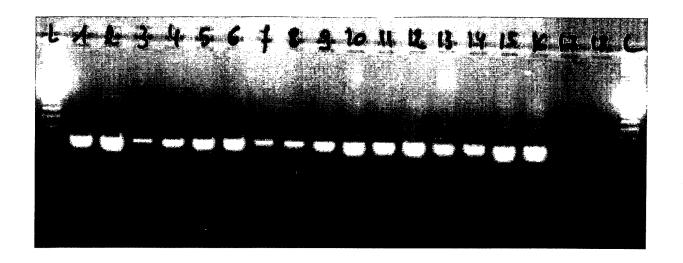


- 1 = DNA Ladder (λ /Hind III)
- 2: Streptococcus pyogenes
- 3. Streptococcus penumoniae
- 4. Streptococcus oralis
- 5. Enterococcus hirae
- 6. Enterococcus casseliflavus
- 7. Streptococcus agalactiae
- 8. Streptococcus sanguis
- 9. Enterococcus faecalis
- 10. Enterococcus gallinarum
- 11. Enterococcus faecium
- 12. Enterococcus flavescens
- 13. Enterococcus durans

- 1': DNA Ladder (λ/Hind III)
- 2': Enterococcus raffinosus
- 3': Enterococcus villorum
- 4': Staphylococcus aureus
- 5': Staph. epidermidis
- 6': Staphylococcus hominis
- 7': Bacillus anthracis
- 8': Bacillus cereus
- 9': Bacillus megatherium

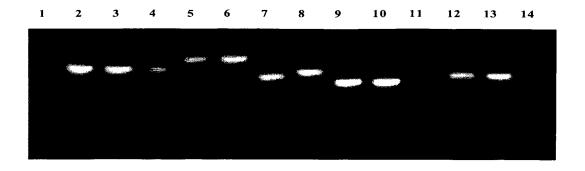
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Figure 2. Amplification of molecular marker II (ptsI) in Gram-positive bacteria



- L = DNA ladder (123 bp)
- 1. Bacillus anthracis
- 2. Bacillus cereus
- 3. Listeria moniocytogenes
- 4. Bacillus subtilis
- 5. Streptococcus peneumoniae
- 6. Streptococcus pyogenes
- 7. Streptococcus agalactiae
- 8. Streptococcus mutans
- 9. Enterococcus faecalis
- 10. Staphylococcus aureus
- 11. Staphylococcus epidermidis
- 12. Bacillus thuringensis
- 13. Staphylococcus hominis
- 14. Enteococcus faecium
- 15. Clostridium perfringens
- 16. Bacillus mycoides
- 17. Negative control
- 18. Negative control

Figure 3. Amplification of molecular marker III (SpyM3_0902- SpyM3_0903) in Gram-positive bacteria



- 1. DNA Ladder
- 2: Streptococcus pyogenes
- 3. Streptococcus pneumoniae
- 4. Enterococcus faecalis
- 5. Streptococcus agalactiae
- 6. Streptococcus sanguis
- 7. Enterococcus casseliflavus
- 8. Streptococcus oralis
- 9. Bacillus anthracis
- 10.Bacillus cereus
- 11. Enterococcus raffinosus
- 12. Enterococcus gallinarum
- 13. Enterococcus flavescens
- 14. Negative control of PCR.

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Figure 4: Marker I (PurA) sequences amplified from different Gram positive bacteria (SEQ ID NOs 1-62), and from a Gram-negative bacterium (SEQ ID NO: 63)

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GTCGAGTATCAGGTATTACTAACCTCTCTGAATTCAATTGATGTTCTTTCAGGGCTTGATACGGTGAAAATTT
GTGTGGCTTATGACCTTGATGGGAAACGTATTGACTATTACCCAGCAAGCCTTGAACAGCTAAAACGTTGTAAAC
CAATCTATGAAGAATTACCGGGCTGGTCTGAAGATATTACAGCTTGTCGTAGCTTAGATGATCTTCCAGAAAATG
CACGTAATTACGTTCGCCGTGTTGGCGAATTGGTTGGTGTTCGTATTTCTACTTTNCTCAGTAGGNCCAGGTC

6. Enterococcus faecium (SEQ ID NO. 6) EFCM

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GTCGTGTATCAGGTATTACTAACCTCTCTCTGAATTCAATTGATGTTCTTTCAGGGCTTGATACGGTTAAGATTT
GTGTGGCTTATGACCTTGATGGGAAACGTATTGACTATTACCCAGCAAACCTTGAACAACTCAAACGTTGCAAAC
CAATCTATGAAGAATTACCAGGCTGGCAAGAGGACATCACAGGTGTTCGTAGCCTTGATGAGCTTCCTGAAAATG
CCCGCAACTACGTTCGTCGTGTTGGAGAATTGGTTGGCGTTCGCATTTCAACCTTCTCAGTTGGGCCAGACC

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CATTAAACTCTATCGACGTTCTAACTGGTATTCCAACACTTAAAATTTGTGTTTGCTTACAAATGCGATGGGAAAG
TTATCGATGAAGTTCCAGCAAACTTAAACATTTTAGCGAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGGA
CAGAAGATATTACTGGTGTAAGATCATTAGATGAGCCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTG
AGTTAACAGGAATTCAATTATCTATGTTCTCAGTG

13. Bacillus anthracis Butare (SEQ ID NO. 13)

14. Bacillus anthracis Sterne (SEQ ID NO. 14)

CTTCGACNCGGTACCGTTCGTTACATCTTCTAACCCAATTGCTGGTGTGAACAGTTGGAACTGGAGTT
GGTCCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCT
ACTGAGCTTCATGACGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACTGGTCGTCCA
CGCCGCGTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAACAGATTTATCATTA
AACTCTATCGACGTTCTAACTGGTATTCCAACACTTAAAATTTGTGTTGCTTACAAATGCGATGGGAAAGTTATC
GATGAAGTTCCAGCAAACTTAAACATTTTAGCGAAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGGACAGAA
GATATTACTGGTGTAAGATCATTAGATGAGCCTTCCTGAAAATGCACGAAAAATACGTAGAACGTGTTTCTGAGTTA
ACAGGAATTCAATTATCTATGTTCTCAGTGGCCCC

15. Bacillus anthracis 1655H85 (SEQ ID NO. 15)

GGTNCGTACCCGTTCGTTACATCTTCTAACCCAATTGCTGGTGTGTAACAGTTGGAACTGGAGTTGGTCCTGCG

AAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTGAGCTT

CATGACGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACTGGTCGTCCACGCCGCGTA

GGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAACAGATTTATCATTAAACTCTATC

GACGTTCTAACTGGTATTCCAACACTTAAAATTTGTGTTGCTTACAAATGCGATGGGAAAGTTATCGATGAAGTT

CCAGCAAACTTAAACATTTTAGCGAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGGACAGAAGATATTACT

GGTGTAAGATCATTAGATGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATT

CAATTATCTATGTTCTCAGTGGCCCCNGGNCCNAN

16. Bacillus anthracis Coda-cerva (SEQ ID NO. 16)

GGTNCGTACCCGTNCGTTACATCTTCTAACCCAATTGCTGGTGGTGTAACAGTTGGAACTGGAGTTGGTCCTGCG

AAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTGAGCTT

CATGACGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACTGGTCGTCCACGCCGCGTA

GGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAACAGATTTATCATTAAACTCTATC

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GACGTTCTAACTGGTATTCCAACACTTAAAATTTGTGTTGCTTACAAATGCGATGGGAAAGTTATCGATGAAGTT
CCAGCAAACTTAAACATTTTAGCGAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGGACAGAAGATATTACT
GGTGTAAGATCATTAGATGAGCCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATT
CAATTATCTATGTTCTCAGTGGCCCCNNGGNCCCA

17. Bacillus anthracis 2054H82 (SEQ ID NO. 17)

18. Bacillus cereus ATCC 10987 (SEQ ID NO. 18) BCER10987

GNCNCGGTACCCGTTCGTTACATCTTCTAACCCAATTGCTGGCGGTGTAACAGTTGGAACTGGAGTTGGTC
CTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTG
AGCTTCATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGCGAGTATGGAACGACAACTGGTCGTCCACGCC
GCGTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAACGGATCTATCATTAAATT
CTATCGACGTTTTAACAGGTATTCCAACTCTTAAAATTTGTGTAGCTTACAAATACAATGGCGAAGTTATTGATG
AAGTTCCAGCTAACTTAAACATTTTAGCGAAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGGAAGAAGATA
TTACTGGTGTAAAAATCATTAGATGAACTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAG
GAATTCAAATATCTATGTTCTCAGTAGNCCCC

19. Bacillus cereus ATCC 14579 (SEQ ID NO. 19) BCER14579

GGTCGTACCCGTTCGTTACATCTTCTAACCCAATTGCTGGTGTGTAACAGTTGGAACTGGAGTTGGTCCTGCGA
AAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTGAGCTTC
ATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGCGAGTATGGAACGACAACTGGTCGTCCACGCCGCGTAG
GTTGGTTCGATAGCGTTGTTAAAACATGCACGTCGTGTTAGTGGTTTAACGGATCTATCATTAAATTCTATCG
ACGTTTTAACAGGTATTCCAACTCTTAAAATTTGTGTAGCTTACAAATACAATGGCGAAGTTATTGATGAAGTTC
CAGCTAACTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGGAAGAAGATATTACTG
GTGTAAAAATCATTAGATGAACTTCCTGAAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATTC
AAATATCTATGTTCTCAGTNGGCCCC

20. Bacillus megatherium (SEQ ID NO. 20) BMEG

CTATTCGAAGGGGCACAAGGTGTTATGTTAGATATCGATCAAGGAACATATCCATTTGTTACATCTTCAAACCCA
GTAGCGGGTGGAGTAACAATTGGTTCTGGGGTAGGTCCATCTAAAATCAAACACGTTGTAGGTGTATCAAAAGCG
TATACAACTCGTGTTGGTGACGGCCCTTTCCCAACTGAATTAACAAACGAAATCGGTGATCAAATCCGTGAAGTA
GGACGTGAATATGGTACAACAACTGGTCGTCCTCGCCGTGTAGGTTCGACAGTGTAGTTGTACGTCATGCT

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CGTCGCGTTAGTGGAATCACAGATCTATCTTTAAACTCAATTGATGTATTAACGGGAATTGAGACATTAAAGATT
TGCGTAGCTTATCGTTATAAAGGGGAAGTTATGGAAGAATTCCCTGCTAGCTTAAAAACACTTGCAGAGTGCGAA
CCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACGGGTGTGAAAACATTAGATGAGTTACCTGATAAC
GCTCGCCACTACTTAGAGCGCGTGTCTCAATTAACAGGTATTCCTTTATCTATTTTCTCAGTAGGTCCAGGCC

- 22. Enterococus raffinosus (SEQ ID NO. 22) ERAF

 CTATTTGAAGGTGCTCAAGGCGTTATGCTGGATATTGATCAAGGAACCTATCCATTTGTTACTTCTTCGAACCCA
 GTTGCCGGTGGGGTAACTATCGGTAGTGGTGTAGGACCTGCTAAAATCGACAAAGTTGTCGGTGTTTGTAAAGCC
 TATACTTCACGCGTAGGTGATGGACCTTTCCCAACTGAATTGTTTGATGAAGTTGGAGATCAGATTCGTGAAGTC
 GGTCGTGAATATGGAACGACTACTGGTCGTCCACGTCGTGTGGGCTGGTTTGACTCGGTTGTGATGCGTCATTCA
 AAACGTGTTTCTGGGATTACGAATCTTTCTTTAAACTCGATTGATGTCTTGAGCGGTCTGGATACAGTGAAAATT
 TGTACAGCGTATGAGCTGGACGGAGAACTAATTTACCATTATCCAGCAAGCCTAAAAGAATTAAATCGTTGTAAG
 CCCGTTTATGAAGAACTACCTGGTTGGAGCGAAGATATTACAGGCTGCCGTGATTTAGCTGATCTACCGGAAAAT
 GCGCGTAATTATGTACGTCGCGTTTCTGAACTTGTGGGTGTGCGTATCTCGACCTTCTCAGTTGGTCCTGGTC

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- TGGCTTGCNATCGACCAAGGTAACTTACCCATTTGTTACTTCTTCAAACCCAGTTGCTGGTGGGGTAACAATCGG
 TTCAGGTGTTGGTCCAAGCAAGATCAATAAAGTTGTCGGTGTGAAATTGGTCACCAAGCCGTGTTGGTGACGG
 TCCGTTCCCAACAGAACTTCTAGATGAAGTTGGAGATCGTTATCCGTGAAATTGGTCACGAATATGGTACAACAAC
 TGGACGTCCACGTCGTGTTGGTTTGACTCAGTTGTTATGCGTCACAGCCGCCGCGTATCAGGTATCACAAA
 CTTGTCACTTAACTCAATCGATGTTCTTTCAGGACTTGATACTGTTAAAATCTGTGTGGCATACGACCTTGACGG
 TCAACGTATCGACCACTACCCAGCAAGTCTTGAACAATTGAAACGTTGTAAACCAATCTACGAAGAATTGCCAGG
 TTGGTCAGAAGACATCACAGGTTGCCGTAGCCTAGATGAACTTCCCGAAAATGCTCGTGACTACGTTCGCCGTGT
 TGGTGAACTCGTTGGTGTTCGCATTTCAACATTCTCAGTTGGCCCC
- 28. Streptococus mutans (SEQ ID NO. 28) SMUT

 TATGGCTTGCNATTGACCAAGGTAACCTATCCATTTGTAACTTCATCAAATCCAGTTGCAGGTGGCGTTACCATC

 GGATCTGGTGTTGGACCAAGTAAAATCAATAAGGTTGTTGGTGTCTGCAAAGCCTATACCAGCCGTGTAGGTGAT

 GGTCCTTTCCCCACAGAACTTTTTGACCAAACGGGAGAGCGCATTCGTGAAGTTGGGCATGAATACGGGACAACA

 ACAGGGCGTCCGCGTCGAGTTGGTTGGTTTGACTCAGTTGTTATGCGTCACAGCCGCCGTGTATCAGGCATTACC

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AATTTATCTCTTAACTGTATTGATGTACTTTCAGGTCTTGATATCGTAAAAATCTGTGTAGCCTATGATTTGGAT
GGAAAACGGATTGATCACCTGCCAGTCTCGAACAACTCAAACGCTGTAAACCTATTTATGAAGAATTGCCG
GGCTGGTCTGAAGATATTACAGGGGTTCGCAGTTTAGAAGATCTTCCTGAAAATGCTCGTAATTATGTCCGCCGT
GTAAGTGAATTAGTTGGTGTTCGTATTTCTACTTTCTCAGTNGTCCCC

- 29. Streptococus gordonii (SEQ ID NO. 29) SGOR

 TAATGCTAGCAATTGACCAAGGTACCTATCCATTTGTAACCTCATCTAATCCAGTTGCTGGTGGTGAACGATCG
 GTTCTGGTGTGGGTCCTAGCAAGATTGACAAAGTAGTGGGTGTTTGTAAAGCCTATACAAGTCGTGTTGGTGATG
 GTCCTTTCCCAACAGAGCTTTTCGATGAAGTAGGTGACCGCATTCGTGAGGTTGGTCATGAGTATGGTACAACAA
 CAGGACGTCCGCGTCGAGTTGGTTTGACTCTGTTGTTATGCGCCATAGCCGCCGTGTATCTGGGATTACCA
 ATCTTTCGCTTAACTCTATCGATGTTTTGAGCGGTCTGGATACAGTCAAGATCTGTGAGCCTATGATTTGGATG
 GCCAAAGAATCGACCACTATCCAGCTAGTTTGGAACAGCTTAAACGTTGTAAGCCGATTTACGAAGAGCTTCCTG
 GATGGTCTGAAGATATTACTGGCGTTCGTAAGTTAGAAGATCTTCCAGAAAATGCTCGCAACTATGTTCGGCGAG
 TAAGCGAGTTGGTTGGTGTACGTATTTCCACCTTCTCAGTTGGCCCC
- 31. Bacillus pumilus (SEQ ID NO. 31)

 GTTATGGCTTGCTATTGATCAAGGGACATATCCATTTGTCACGTCATCTAACCCAGTAGCTGGAGGAGTGACGAT
 TGGTTCTGGCGTAGGACCAACAAAAATTCAACATGTGGTCGGCGTGTCAAAAGCGTACACAACACGTGTTGGAGA
 TGGCCCATTCCCGACAGAACTCCATGATGAAATTGGCGATCAAATCCGTGAGGTTGGCCGTGAATACGGTACAAC
 AACTGGACGTCCGCGCGTGTTGGCTGGTTTGACAGTGTCGTTGTCCGTCATGCTCGACGTGTGAGCGGGATTAC
 AGATCTATCTCTTAACTCAATTGATGTACTGACAGGGATTGAAACATTGAAAATCTGTGTCGCTTATAAATTGAA
 CGGAGAAATCACAGAGGAATTCCCAGCAAGTCTAAATGAACTAGCGAAATGTGAGCCTGTCTACGAAGAAATGCC
 AGGATGGACAGAGGATATTACAGGCGTGAAGAATTTAAGCGAACTGCCTGAAAATGCCCGTCATTATTTAGAGCG
 CATTTCACAATTAACAGGTATTCCACTTTCCATTTTCTCAGTTGNCCCC

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ATTCGATTGATGTATTAAGCGGATTAGAAACAGTAAAAATTTGTACGGCCTATGAACTAGATGGTGAGCTGATTT
ATCATTACCCAGCAAGTTTGAAAGAATTGAAACGTTGTAAACCAGTATATGAAGAACTACCTGGATGGTCTGAAG
ATATTACGAAATGCAAGACACTTTCTGAATTGCCAGAAAATGCACGTAACTATGTAAGACGTATTTCTGAGCTTG
TAGGTGTACGCATCTCCACATTTCTCAGTGGNCCC

33. Bacillus thuringiensis serovar israelensis BTHUISR (SEQ ID NO. 33)

CNCGGTACCCGTTCGTTACATCTTCTAACCCGATTGCGGGTGGTGTAACAGTTGGAACTGGAGTTGGCCCT
GCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTTGGTGACGGTCCATTCCCTACTGAA
CTTAATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTACGGAACAACAACTGGTCGTCCGCGCCGC
GTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCGCGTCGTGTTAGTGGTTTAACGGATCTATCATTAAATTCT
ATCGACGTTCTAACAGATATTCCAACTCTTAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAA
GTTCCAGCAAACTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATT
ACTGGTGTAAAAATCATTAGACGAGCTTCCTGAAAATGCAAGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGA
ATTCAATTATCTATGTTCTCAGTGGCCCC

34. Bacillus thuringiensis serovar kurstaki BTHUKUR (SEQ ID NO. 34)

GGTCGTATCCATTCGTTACATCTTCTAACCCAGTTGCTGGTGGTGTAACAATCGGTTCTGGAGTTGGTCCTTCTA
AAATCAATCGTGTAGTAGGCGTATGTAAAGCATATACAAGCCGTGTTGGTGACGTCCATTCCCTACTGAACTTA
ATGATGAAATTGGCCATCAAATTCGTGAAGTTGGTCGTGAATATGGTACAACAACAGGTCGTCCACGTCGCGTAG
GTTGGTTTGACAGCGTTGTTGTAAGACATGCACGCCGTGTGAGTGTTTAACAGATTTATCTTTAAACTCTATCG
ACGTATTAACAGGTATTCCAACTGTGAAAATCTGTATTGCATATAAGTATAATGGAGAAGTTCTGGATGAAGTTC
CAGCAAACTTAAACATTTTAGCAAAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACTG
GTGTAAAATCATTAGAGGAGCTTCCTGAAAATGCAAGACATTATGTAGAGCGTGTCTCAATTAACAGGTATCC
AATTATCTATGTTCTCAGTTGNCCCCC

- 35. Bacillus mycoïdes MYCOO3 (SEQ ID NO. 35) BMYCOO3

 GGTNCGTACCCATTCGTTACATCTTCTAACCCGATTGCTGGTGTGTAACAGTTGGAACTGGAGTTGGTCCTGCG

 AAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTAGGTGATGGTCCGTTCCCTACTGAGCTT

 CATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAATACGGAACAACAACTGGTCGTCCACGCCGCGTA

 GGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAACAGATCTATCATTAAATTCTATC

 GACGTTCTAACAGGTATTCCAACTCTTAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAAGTT

 CCAGCAAACTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACT

 GGTGTAAGAGCATTAGACGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATT

 CAATTATCTATGTTCTCAGTGGNCCCCCGG
- 36. Bacillus mycoïdes NRS306 (SEQ ID NO. 36) BMYC306
 CGGTNCGTACCCGTTCGTTACATCTTCTAACCCGATTGCTGGTGTGAACAGTTGGAACTGGAGTTGGTCCTGC
 GAAAGTTACTCGCGTTGTAGGTGTGTAAAGCATATACAAGCCGTGTAGGTGATGGTCCATTCCCTACTGAGCT

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TCATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACTGGTCGTCCACGCCGCGT
AGGTTGGTTCGATAGCGTTGTTAGAAACATGCACGTCGTGTTTAGTGGTTTAACAGATTTATCATTAAATTCTAT
CGACGTTCTAACAGGTATTCCAACTCTTAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAAGT
TCCAGCAAACTTAAACATCTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGGAAGAAGATATTAC
TGGTGTAAAATCATTAGACGAACTTCCTGAAAATGCAAGAAAATACGTAGAGCGTGTTTCTGAATTAACAGGAAT
CCAATTATCTATGTTCTCAGT

- 37. Bacillus weihenstephanensis (SEQ ID NO. 37) BWEI

TTACCAGGATGGGAAGAAGATATCACTGGTTGCCGTACATTAGAAGAATTACCAGATAACGCACGTAAATACTTA

GAACGCATTTCTGAATTATGTAATGTACGTATTTCAATCTTCTCAGT

- 40. Bacillus subtilis (SEQ ID NO. 40) BSUB
 CTCAAGGGGTTATGCTTGATATTGACCAAGGGACATACCCGTTTGTCACTTCATCCAACCCGGTCGCCGGAGGGG
 TGACGATCGGTTCAGGCCTAGGCCCGACAAAAATCCAGCACGTCGTCGTTGTATCTAAAGCGTACACAACCCGTG

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TCGGTGACGGTCCTTTCCCGACTGAGCTGAAAGATGAAACCGGGGATCAAATCCGTGAAGTCGGACGCGAATACG
GCACAACGACAGGCCGTCCGCCGCGTGTCGGCTGGTTTGACAGCGTTGTTGTCCGCCATGCCCGCCGCGTCAGCG
GAATCACAGATCTTTCTCTGAACTCAATCGATGTGCTGACTGGCATTGAAACATTGAAAATCTGTGTCGCTTACC
GCTACAAAGGTGAAGTGATTGAAGAATTCCCGGCAAGTCTGAAAGCTCTCGCAGAGTGTGAACCGGTATATGAAG
AAATGCCTGGCTGGACGGAAGATATCACAGGCGCAAAAACATTAAGCGATCTTCCTGAAAATGCGCGCCATTATC
TGGAACGCGTGTCTCANCTGACAGGTATTCCGCTTTCTATTTTCTCAGTAGGTCCAGA

- TNATGCTTGATATTGACNAGGAACATACCCATTTGTAACTTCTCAAACCCAGTAGCTGGTGGGGTAACGATTGGC
 TCTGGTGTGGGGTCCATCAAAAATTTCAAAAGTTGTTGGTGTTTGTAAAGCCTATACTTCACGTGTGGGTGATGGT
 CCATTCCCAACAGAACTTTTTGATGAAGTTGGACATCAAATTCGTGAAGTAGGACATGAATATGGAACAACA
 GGACGTCCACGTCGTGTTGGTTTGATTGACTCAGTCGTAATGCGTCATGCAAAACGTGTTTCTGGCTTGACAAAT
 CTTAGCTTGAATTCAATTGACGTTCTCTCAGGACTTGAAACAGTAAAAATTTGTGTTGCTTACGAACGTAGTAAT
 GGTGAACAAATTACTCATTATCCAGCATCACTTAAGGAATTAGCAGATTGCAAACCAATCTATGAAGAATTGCCA
 GGATGGTCTGAAGATATTACTTCATGCCGAACTTTAAGAAGAGTTACCAGAAGCTGCTCGTAACTATGTTCGTCGG
 GTTGGTGAACTAGTTGGCGTACGTATCTCGACTTTCTCAGTNGTCCCC
- 44. Enterococus avium (SEQ ID NO. 44) EAVI
 CTTTTCGAAGGTGCGCAAGGTGTAATGCTGGATATTGATCAAGGGGACTTATCCATTTGTTACCTCTTCTAATCCG
 GTTGCCGGCGGTGTCACGATCGGTAGCGGTGTTGGACCATCGAAGATTGATAAAGTCGTAGGGGTATGTAAAGCT

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TATACATCACGCGTTGGTGATGGACCTTTTCCAACGGAATTATTTGACGAAGTCGGCGATCAGATCCGCGAAGTT
GGTCGTGAATATGGAACAACAACTGGCCGTCCACGTCGAGTTGGCTGGTTTGACTCTGTGGTTATGCGGCACTCA
AAACGCGCTTCTGGGATTACCAATCTATCTTTGAACTCAATCGATGTGTTGAGCGGCTTGGAAACGGTCAAGATT
TGTACCGCTTATGAGTTAGACGGAGAATTAATCTATCATTATCCAGCAAGCTTAAAGGAATTGAATCGCTGCAAA
CCAGTTTATGAAGAGCTACCTGGCTGGAGTAAGGATATTACTGGCTGTCGTGATT

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49. Staphylococcus capitis capitis (SEQ ID NO. 49) SCAPCAP

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- TTCTTTGAAGGAGCTCAAGGTGTTATGTTAGATATTGATCATGGTACATATCCTTTCGTCACATCAAGCAATCCT
 GTAGCCGGCAATGTCACTGTTGGTACAGGTGTAGGTCCAACCTTCGTTTCTAAAGTAATTGGTGTGTAAAGCA
 TACACATCTCGCGTAGGCGATGGTCCTTTCCCAACCTGAACCTATTTGATGAAGATGGGCACCATATTAGAGAGGTT
 GGTCGTGAATATGGTACGACGACAGGACGTCCACGTCGCGTGGGTTTGATTCAGTCGTGCTACGTCACTCA
 CGTCGTGTTAGTGGTATACAGACTTATCTATTAACTCTATTGATGTACTAACAGGTTTAGATACGGTAAAAATT
 TGTACAGCTTATGAGTTAGATGGAGAAGAAATTACGGAGTATCCAGCTAACCTTGATCAATTAAAACGTTGTAAA
 CCAATCTTTGAAGAATTACCTGGTTGGACAGAAGATATTACAGGCTGTCGTTCATTAGAAGCATTGCCTGATAAT
 GCACGTCGCTATTTAGAACGTATTTCAGAATTATGCGGCGTTCATATTTTCAATTTTCTCAGTAGGGCCAGACCA

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56. Staphylococcus cohnii urealyticum (SEQ ID NO. 56) SCAPURE

CTCGTTGAAGGTGCACAAGGCGTTATGTTAGATATCGACCACGGTACATACCCATTCGTTACGTCAAGTAACCCA
GTTGCAGGTAATGTCACTGTCGGTGGTGTTTGGTCCAACATACGTATCTAAAGTCATTGGCGTATGTAAAGCT
TATACATCACGTGTCGGTGATGGCCCATTCCCAACAGAACTATTTGATGATGATGACACCACCACCACCCTGGAAATT
GGCCGTGAGTACGGTACAACTACTGGACGTCCACGTCGTGTAGGTTCGATTCAGTTGTATTACGTCACTCT
CGTCGTGCGAGTGGTATTACTGATTTATCAATCAACTCTATCGATGTCTTAACAGGCCTTAAAGAAGTGAAGATT
TGTACGGCGTATGAATTGGACGGTAAAGAAATTACTGAATATCCAGCGAATTTAAAAGACTTACAACGTTGTAAG
CCAATCTTTGAAACATTACCTGGTTGGACAGAAGATGTTACAGGTTGTCGCTCATTAGATGAGCTGCCAGACAAT
GCACGTAGATATTTAGAACGTATCTCTGAATTATGTGACGTTCCAAATTTCAATCTTCTCAGTAGGGCCTGACCA

57. Staphylococcus xylosus (SEQ ID NO. 57) SXYL

CCAATTTACGAAGAATTACCAGGTTGGTCTGAAGATATTACAGGCGTACAATCATTAGAAGAATTACCAGATAAC GCACGTCGTTACTTAGAACGTATTTCTGAGTTATGTAACGTAGGTATCTCAATCTTCTCAGTTGGTCCAGGTCA

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Figure 5. Molecular marker II (ptsI) sequences amplified from Gram positive bacteria (SEQ ID NOs: 64-107; SEQ ID NOs: 109-111, SEQ ID NOs: 117-129, SEQ ID NO: 137, SEQ ID NOs 145-148), from some Gram-negative bacteria (SEQ ID NOs 108, 112-116, 130-136, 138-144) and from the fungi Cryptococcus neoformans (SEQ ID NO: 149).

64. Bacillus anthracis 1978 (SEQ ID NO. 64)

65. Bacillus anthracis butare (SEQ ID NO. 65)

66. Bacillus anthracis sterne (SEQ ID NO. 66)

67. Bacillus anthracis 1655H85 (SEQ ID NO. 67)

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68. Bacillus anthracis Coda-Cerva (SEQ ID NO. 68)

69. Bacillus anthracis 2054H82 (SEQ ID NO. 69)

70. Bacillus cereus ATCC 10987 (SEQ ID NO. 70)

71. Bacillus cereus ATCC 14579 (SEQ ID NO. 71)

72. Listeria monocytogenes (SEQ ID NO. 72)

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TACTGTTGCAATCATCGGGAACATAATTTTTAAGTTACCATATACACTTGCGCGAAGTAAGGCGCGAAGTTGCGT ACGGAATAATTCTTCATTCGCAAAACAAAGACGAATTGCGCGGAATCCCCAAGAACGATCNTTCTCCTTA

- 75. Streptococus agalactiae (SEQ ID NO. 75)

 GAGCAGCTTTGATAACGTTGTTAATCAAACGAAGGATTGATGGATTGTATGGTTGATAGAGGTATGAAACTTGCT
 CATTCATACGGTCCGCAGCCATTGTGTATTGGATAAGATCATTAGTACCAATTGAGAAGAAATCAACTTCTTTTG
 CAAATTGGTCTGCAAGCATAGCTGCCGCTGGGATTTCAATCATAATACCAACTTCAATGCCTTCAGCTACTGCTA
 CACCGTCAGCTAACAAGTTCGCTTTCTCTTCTAAATATAGCTTTAGCAGCACGGAATTCTTTAAGCAAAGCAA
 CCATTGGGAACATGATGCGTAGCTGTCCATGAACTGAAGCACGAAGAAGTGCTCGGATTTGTGTGCGGAACATTG
 CATCACCAGTTTCAGAAATTGAAATACGCAATGCACGGAATCCCAAGAACGGATCNTTTTTCNTA

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80. Bacillus thuringiensis serovar israelensis BTHUISR (SEQ ID NO. 80)

81. Bacillus thuringiensis serovar kurstaki BTHUKUR (SEQ ID NO. 81)

82. Staphylococcus hominis (SEQ ID NO. 82) SHOM
CNCCNNCCTTATGAGGAAGCTTCAATAACCTGTTTAACTAAACGTAAAATTGCTGGATTATATGGTTGATATAAA
TATGAAACACGTTCAGACATACGATCAGCTGCCATAGTATATTGAATTAAGTCATTAGTTCCTATACTAAAGAAA

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- 84. Clostridium perfringens (SEQ ID NO. 84) CPER
 CNTGTTGGAGCTCCATCTATTGTCATTTTGATTAATCTTAATACAGCTGGATGCATTGGATTGTAAAGGTATG
 ATACCTTTTCACTCATTCTGTCAGCAGCTAATGTATATTGTATTAAATCGTTAGTTCCTATTGAGAAGAAATCAA
 CATGCTTAGCTAATTCATCAGCATAAACTGCTGCAGCTGGGATTTCAACCATGATACCCCATTGAATTGAATCTG
 AGTATGCTATACCTTCTGCTTTTAACTCAGCTTTGCATTCTTCAACAAATGCTTTAGCTTGTTGGAATTCTTCTA
 ATCCTGAAATCATTGGGAACATTACTGCAAGATTTCCATAAACAGAAGCTCTTAATAAAGCTCTTATTTGAACTC
 TAAAGATATCTTTTCTGTCTAAGCATAATCTTATAGCTCTGTATCCCAAGAACGGATCNNTNNTCNTTAA

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- 87. Streptococus oralis (SEQ ID NO. 87) SORA
 CNNTTTCCCTTCGCGTGAGCTGCTTTGATAACGTTGTTGATCAGCGTAGGATTGATGGGTTGTATAGGTTGGTAAA
 GGTATGAAACTTGCTCGTTCATACGGTCTGCTGCCATTGTGTATTGGATCAAGTCGTTTGTACCAATTGAGAAGA
 AGTCAACTTCTTTAGCAAATTGGTCTGCAAGCATTGCTGCTGCAGGAATTTCGATCATGATACCAACTTGGATAT
 TATCCGCAACTGCAACACCTTCAGCAAGAAGGTTTGCTTTTTCTTCGTCAAAGACTGCTTTCGCTGCACGGAATT
 CTTTCAAGAGCGCAACCATTGGGAACATGATACGTAATTGACCGTGAACAGACGCACGAAGAAGAGCACGGATTT
 GTGTGCGGAACATAGCATCTCCAGTCTCAGAGATAGAGATACGAAGAGCACGGAATCCNAAGAACGGATCNTTTC
 TCTTA
- 88. Enterococus hirae (SEQ ID NO. 88) EHIR
 CNATTTACCTTCGCATGCGCTGCATCGATCACGTTTTTAATCAAACGTAGGATTGATGGGTTGTAAGGTTGATAC
 AAGTATGAAACACGTTCGTTCATACGGTCAGCTGCCATAGTGTATTGGATCAAGTCATTCGTTCCTACTGAGAAG
 AAGTCAACTTCCTTAGCAAACTTGTCAGCTAAGACAGCTGCTGCTGGAATTTCGATCATGATGCCGACTTGGATC
 GTATCAGATACTTCCACGCCTTCATTCAATAATTTTTGTTTTTCGTCTTCAAAGATTGCTTTTGCAGCACGGAAT
 TCTTTAAGAGTCGCTACCATTGGGAACATGATACGTAAGTTTCCATGAACAGATGCACGTAATAATGCGCGCATT
 TGCGTACGGAACATTTCGTCACCTTGTTCTGACAAGCTGATTCGTAATGCACGATAGCCCAAGAACGGATCNTTN
 TCCTTA
- 90. Staphylococcus saprophyticus (SEQ ID NO. 90) SSAP

 TCGTAAGAAGCTTCTATTACTTGTTTTACTAAACGTAATATTGAAGGATTATATGGTTGATACAAGTAAGAAACA

 CGTTCTGACATTCTATCAGCAGCCATTGTATATTGAATTAAATCATTCGTTCCTATACTGAAGAAATCAACTTCT

 TTAGCAAATACATCTGCCAACGCAGCAGTAGAAGGAATTTCTACCATAATACCAAGTTCGATATCATCAGAAACT

 TCAATGCCTTCATTTGTTAAGTTATCTTTTTCTTCAAGTAACAATGCTTTAGCATCACGGAACTCTTGGATTGTA

 GCTACCATAGGGAACATGATATTCAATTTACCAAAAGCAGATGCACGTAATAATGCACGCAACTGTGGTCTGAAA

 ATATCAGGTTGATCTAGGCATAAACGGATAGCACGGTAACCCAAGAACGGATCATTCTCTTA

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 ${\tt TTGGGAACATAATGTTTAATTTACCGTAAGCTGACGCGCGTAATAATGCACGTAATTGTGTTCTGAAAATATCTT}\\ {\tt GTTGATCTAAGCATAGACGAATTGCTCTGTAACCCAAGAACGGNTCNTTCTCTTA}\\$

- 96. Enterococus villorum (SEQ ID NO. 96) EVIL

 GGNCTCTCGTCGTNAGCTGCATCAATCACGTTTTTGATTAAACGTAAAATTGATGGGTTATAAGGTTGGTATAAG

 TATGAAACGCGTTCGTTCATACGGTCAGCTGCCATAGTGTATTGAATCAAATCATTTGTTCCTACTGAGAAGAAG

 TCAACTTCCTTCGCAAACTTGTCAGCTAAAACAGCAGCTGCAGGAATTTCAATCATAATGCCGACTTGGATCGTA

 TCAGATACTTCCACGCCTTCATTCAATAACTTTTGTTTTTCATCTTCAAAGATTGCTTTTGCCCCACGGAATTCT

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- 97. Clostridium difficile (SEQ ID NO. 97) CDIF

 TTTNNGGANGGCNTCTNTCGTANGCATTGTCTATANCAGTCTTTATAAGTCTTAAAACAGCTGGATNAAATTGAT

 TGTAAAGNTAACTTATCTTTTGATTCATTCTATCAACTGCACAAGTGTATTGAATTAAATCATTAGTTCCTATAG

 AGAAGAAATCTACGTGTTTAGCCAATACATCAGATATCACAGCAGCAGCAGATGGAACTTCTATCATCATACCAATTT

 CTACATCTTTAGCATAAGCCACACCTTCAGAATCAAGTTCTGCTAAAACTTCTTTACAACTTCTTTAGCTTGTA

 ACAACTCTTCTAAAGATGAAATCATTGGGAACATGATTCTTAATCTTCCATGAACACTAGCTCTATATAAAGCTC

 TCAATTGAGTCTTAAATATATCTTTTCTATCTAGGCAAAGTCTTATTGCTCTGTAACCCAAGAACGG

- 101. Streptococus species (SEQ ID NO. 101) SSPE

 CNNANTTNCCTTCGCGTGAGCTGCTTTGATAACGTTGTTAATCAACGAAGGATTGATGGGTTGTATGGTAA

 AGGTATGAAACTTGTTCGTTCATACGGTCAGCAGCCATTGTGTATTGGATAAGGTCGTTTGTTCCGATTGAGAAG

 AAGTCAACTTCTTTCGCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTGGATA

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TCATCTGAAACGGCAACACCTTCAGCTTTAAGGTTTGCTTTTTCTTCATCAAAGATTGCTTTAGCAGCACGGAAT
TCTTTAAGAAGAGCAACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATT
TGTGTACGGAACATTGCATTTCCTGTTTCTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGATCCTTT
TTCCTTAA

- NTGCCTTCGCATGAGCCGCCTTGATAACATTGTTGATCAAGCGAAGGATAGATGGGTTATAAGGTTGATAGAGGT
 AAGAGACTTGTTCATTCATCCGGTCAGCTGCCATAGTGTACTGGATCAAGTCGTTGGTACCAATTGAGAAGAAGT
 CAACTTCCTTGGCAAATTGATCCGCCAACATAGCTGCTGCTGCTGGAATTTCAATCATGATACCCACTTGAATGTTAT
 CCGCTACAGCAACACCTTCAGCTTGCAATTTCGCTTTTCTTCTTCGTAAACTGCTTTAGCCTTACGGAATTCTG
 TTAGAAGGGCTACCATTGGGAACATGATACGTAATTGTCCATGTACAGACGCCACGTAAGAGAGCGCGGATTTGTG
 TACGGAACATAGCATTACCAGTTTCAGAGATAGAGATACGCAAAGCACGGAAGCCNAAGAACGGTCNTTTT
- 104. Bacillus pumilus (SEQ ID NO. 104)

 CNTACGCTGCTTCATAACAAGCGTAATCAAACGTAAAATCGCTGGATTGTAAGGCTGGTAAAGATAAGACACTCG
 TTCGTTCATTCGATCAGCAGCCATTGTGTATTGAATCAAATCATTTGTTCCAATACTGAAGAAATCAACTTCTTT
 TGCGAATTGGTCTGCGATGACAGCGGTTGATGGAATTTCTACCATTATACCGATTTCAATGGAATCGGATACGTC
 TGTACCAGCGGCAACCAATGCTTCTTTTTCTTCAAGTAAAATGGCTTTTTGCTTCTCTAAATTCTGATAATGTCGC
 GATCATAGGGAACATGATTTTCAAGTTTCCATATGTACTTGCACGAAGTAAGGCGCGTAGTTGTGTTCTGAAAAT
 CTCCTGTTCTTCGAGGCCAAAGGCGGATCGCTCTAAAGCCNAAGAACGGATNTTTTTCNTTAA

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(SEQ ID NO. 106) 106 Lactococcus lactis LLAC GTGAGCTGCTTTGATNCATTGTTAATCAAACGAAGGATTGATGGATTGTAAGGTTGGTAAAGGTAAGAAACTTGT TCATTCATACGGTCTGCAGCCATTGTATATTGGATGAGGTCGTTTGTACCAATTGAGAAGAAATCAACTTCCTTA GCAAATTGGTCTGCAAGCATTGCTGCTGCTGGAATTTCAATCATGATACCTACTTCGATACCATCTGCAACTGGA ACACCTTCAGCAATCAATTTTGCTTTTTCTTCGTCATAAATCTTCTTAGCTGCACGGAACTCAGTTACGAGAGCA ACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGAAGCACGCAAGAGTGCACGCAATTGTGTACGGAACATT CCGTCACCAGCTGTTGAAAGGCTGATACGAAGTGCACGCCATCCCANGAACGGTNNTTTTTTTTAA

- 107. Bacillus firmus (SEQ ID NO. 107) BFIR TCCAGGANGGGTTCTNTCNTANGCTGCGTCAATTACCATTTTAACTAAACGCAGGATTGCAGGATTATACGGCTG GTAAAGGTAAGAAACACGCTCATTCATGCGGTCTGCAGCCATTGTGTACTGAATTAGATCATTAGTGCCAACACT GAAGAAATCGACTTCTTTAGCAAACTGATCAGCCATAACAGCAGTTGAAGGAATTTCAACCATAATTCCAATTTC AATGTTGTCGGCAACCTCTGCTCCTTCGCTCACAAGCTTTTGTTTTTCTTCTTCAAGGATTGCTTTGCCCTGACG TAATTGCGTCCTGAACATATCCTGTTCTTCCAGACACAGACGAATCGCCCGGAAGCCCAAGAACGGATTCATTNT CTTA
- Haemophilus influenzae (SEQ ID NO. 108) HINF TGAGAGGCATCAATCACTTGTTTAATTAAACCAAGCACAGAGGGGTGCATCGGATTATAAAGATGGGAAATAAAC TCATTACCGCGATCTACAGCCAAAGTATATTGAGTTAAATCGTTAGTACCGATACTAAAGAAATCCACTTCTTTT GCTAAAAATTTTGCATTTACTGCGGCAGAGGGGGTTTCGACCATTACACCCAACTTGGATATTATTATCAAACAGT CTCCCCTCTCACGTAATTCCGCTTTTAATGTTTCAATAACCGCTTTTAATTCCCGAATTTCTTCTACAGAAATA ATCATCGGGAACATTACCGCCAATTTACCAAAAGCTGAAGCACGTAACACCGCGCGTAATTGTGCATTTAAAATT TCACGACGATCTAATGCAATGCGAATCGCACGCCATCCCAAGAACGGATNNTTTTTCTT

108.

109. Streptococcus bovis (SEQ ID NO. 109) SBOV ${\tt TCATTCATACGGTCAGCCATTGTGTATTGGATAAGGTCGTTTGTTCCGATTGAGAAGAAGTCAACTTCTTTT}$ GCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTGGATATCATCTGAAACGGCA ACACCTTCAGCTTTAAGGTTAGCTTTTTCTTCATCAAAGATTGCTTTAGCAGCACGGAATTCTTTAAGAAGTGCA ACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATTTGTGTACGGAACATT GCATTTCCTGTTTCTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGTCCNTTTTTNCTTA

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- 113. Serratia liquefasciens (SEQ ID NO. 113) SLIQ

 NTGNCTTCTGCATGAGNATGCATCAATAACCTGTTTGATCAGGCCAAGCACTGATGGGGACATCGGGTTATAGAG

 ATGAGAAATCAGCTCATTGCCGCGATCTACCGCCAGAGTATACTGGGTTAGATCGTTTGTCCCAATACTAAAGAA

 GTCGACTTCTTTCGCCAGGTGATGAGCAATCACTGCCGCGGCCGGTGTTTCCACCATTACGCCCACTTCAATGGT

 CTCGTCAAAAGGCCTTGGATTCTTCACGCAGCTGCGCCTTCAGCGTCTCGATTTCACCTTTCAGATCGCGGACTTC

 TTCCACGGAAATGATCATCGGGAACATGATGCGCAGTTTGCCGAACGCGGAAGCGCGCAGGATGGCGCCAGTTG

 CGCGTGCAGGATTTCTCTGCGGTCCATGGCGATACGAATCGCGCGCCCAGCCNAAGAACGNTTNTTTTANTTTA
- 114. Proteus mirabis (SEQ ID NO. 114) PMIR

 GTGTGATGCATCAATCACCTGTTTAATCAGATTAAGTACAGCAGGTGACATTGGATTATATAGATGAGATATCAG

 CTCATTTCCACGGTCTACAGCCAGAGTATATTGTGTTAGATCGTTAGTCCCAATACTGAAAAAGTCAACTTCTTT

 TGCCATATGGCGAGCCATAACAGCCGCTGCTGGCGTTTCAACCATAACACCGACTTCGATAGATTCATCAAAAGG

 CTTATTTTCTTCACGAAGCTGGCTTTTCAGTATTTCAAGTTCCGCTTTCAATGCTCGGATCTCTTCAACAGAGAT

 AATCATTGGAAACATAATACGTAGTTTACCAAAAGCAGACGCTCTTAAGATAGCACGTAATTGTGGATGAAGGAT

 CTCTTTGCGGTCAAGACAAATACGAATTGCACGCCAACCCCAAGAACGGATCNTTTNTCCTT

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- 117. Staphylococcus simulans (SEQ ID NO. 117) SSIM

 TTCTCCGCACATACCTGTCCATTTACCTTCAGCATGAGACGCTTCGATAACACGTTGTACCAAGCGTAAAATAGC

 TGGGTTATATGGTTGGTATAAATAAGACACACGTTCTGACATACGGTCAGCTGCCATTGTATATTGGATTAAGTC

 ATTTGTTCCGATACTGAAGAAGTCTACTTCTTTCGCAAAGACATCAGCAAGTGCTGCTGTCGATGGAATTTCAAC

 CATGATACCGACTTCGATATCATCTGAAACTTCAACACCTTCATTTTTAAGGTTTTTAATTTTTCCGTATACTGAAGC

 ACGTAATAACGCGCGTAATTGCGGACGGAAAATTTCTGGTTGTGCTAAGCACAAGCGGATTGCACGATAACCCAA

 GAACGGAT
- 118. Staphylococcus sciuri (SEQ ID NO. 118) SSCI
 CTCCGCACATACCAGTCCATTTACCTTCTTTATGAGAAGCTTCAATTACTTGCTTAACTAAGCGAAGAATTGCAG
 GGTTATATGGTTGGTATAAGTAAGAAACACGCTCAGACATACGGTCAGCAGCCATTGTATATTGGATTAAATCAT
 TCGTACCAATACTGAAGAAATCAACTTCTTTAGCAAAGATGTCTGCAAGTGCTGCAGTAGATGGAATTTCTACCA
 TAATACCGATTTCGATATCATCCGCAACGTTAACACCTTCAGAAACTAATTTTTCTTTTTCCTCAAGTAAGATTG
 CTTTAGCATCTCTAAATTCTTTAATAGTTGCAATCATAGGGAACATGATATTTAACTTACCAAATTCAGATGCGC
 GTAATAAAGCTCTTAATTGTGTTCTAAAGATTTCAGTTTGATCTAAACATAAACGAATCGCTCTATATCCCAAGA
 ACGG
- 119. Staphylococcus capitis capitis (SEQ ID NO. 119) SCAPCA
 TCCGCACATACCAGTCCATTTACCTTCTTTATGAGAAGCTTCAATGACTTGCTTAACAAGACGTAATATAGATGG
 GTTATATGGTTGATATAAATAAGATACACGCTCTGACATACGATCAGCAGCTAGTGTATATTGAATTAAATCATT
 TGTACCAATACTAAAGAAATCTACTTCCTTCGCAAAGACATCTGCTAATGCAGCAGTTGCTGGAATTTCAACCAT
 GATACCTAATTCAATATCATCAGAAATGTCATAACCTTCATTTTCAAGGTTTTTCTTTTCCTCTAAAAGAATTGC

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- 120. Staphylococcus warneri (SEQ ID NO. 120) SWAR

 CCGCACATACCAGTCCATTTACCTTCTTTGTGAGAAGCTTCAATGACTTGTTTTACTAAGCGTAAAATTGAAGGG

 TTGTATGGTTGATATAAGTAAGATACACGTTCAGACATACGGTCAGCTGCTAATGTGTATTGGATTAAGTCATTT

 GTACCAATACTAAAGAAATCTACTTCTTTAGCAAAATACATCAGCTAATGCTGCTGTCGCTGGTATTTCAACCATG

 ATACCTAACTCAATATCTTCAGAAACTTCATAACCTTCATTTTGAAGATTTTTATTTTACCATAAACTGATGCACGT

 AATAACGCGCGTAATTGTGGTCTGAAAATATCAGGTTGAGCTAAGCAAAGACGAATCGCTCTGTATCCCAAGAAC

 GGATCATTCTCTTA
- 122. Staphylococcus schleiferi scheiferi (SEQ ID NO. 122) SSCH
 CCGCACATACCTGTCCATTTACCTTCTTTATGAGATGCTTCAATTACTTGCTTAACTAAGCGTAAAATTGAAGGA
 TTGTAAGGTTGGTAAAGATATGATACACGTTCTGACATACGGTCAGCTGCCATCGTATATTGAATTAAGTCATTC
 GTTCCAATACTAAAGAAGTCAACTTCTTTAGCAAAAACATCAGCTAAAGCTGCTGTAGATGGAATTTCCACCATA
 ATACCTAACTCAATATCATCGCTAACTTCAACGCCTTCTTGTTTTAAGTTTTCTTTTTTCTTCAAGAAGAAGCGCT
 TTTGCATCGCGGAATTCTTTAATCGTCGCAACCATTGGGAACATAATGTTCAGTTTTCCGTAAGTTGAAGCGCGT
 AATAACGCTCTTAATTGTGGACGGAAAATTTCAGGTTGATCTAAACAAAGACGAATTGCACGGTATCC

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- 125. Staphylococcus capitis uralyticus (SEQ ID NO. 125) SCAPURA
 CCGCACATACCAGTCCATTTACCTTCTTTATGAGAAGCCTCTATTACTTGCTTAACAAGACGTAAAATAGAAGGA
 TTATATGGTTGATATAAATAAGATACACGTTCTGACATACGATCAGCAGCTAGTGTGTATTGAATTAAGTCATTA
 GTACCGATACTAAAGAAGTCTACTTCCTTCGCAAAGACATCTGCTAATGCAGCAGTTGCTGGAATTTCAACCATG
 ATACCTAATTCGATATCGTCAGAAATGTCATAACCTTCATTTTCAAGGTTTTTCTTTTTCTTCTAAAAGAATCGCT
 TTAGCATCACGGAATTCTTTGATAGTAGCAACCATTGGGAACATGATATTTAATTTACCGTAAGCAGATGCACGT
 AATAATGCACGTAATTGCGGTCTGAAAAATATCTTGTTGCGCTAAACATAAACGAATTGCTCTATAACCCAAGAAC
- 126. Staphylococcus gallinarum (SEQ ID NO. 126) SGAL

 CCGCACATACCTGTCCATTTACCTTGTTTAACTAAACGTAAAATTGAAGGATTATATGGTTGATACAAGTATGAT

 ACACGTTCTGACATTCTATCTGCAGCCATAGTGTATTGAATTAAATCATTTGTACCGATACTAAAGAAGTCAACC

 TCTTTAGCAAATACATCAGCTAAAGCTGCTGTAGAAGGAATTTCTACCATGATACCTAATTCGATATCATCAGAT

 ACTTCAACACCTTCTTGTGTTAAATTGTCCTTCTCTTCAAGAAGTAATGCTTTGGCATCACGGAACTCTTGAATT

 GTAGCAACCATTGGGAACATGATATTTAACTTACCGAATGCAGATGCGCGTAATAATGCACGCAATTGCGGTCTG

 AAAATATCAGGTTGATCCAAGCATAAACGTATCGCACGATATCCCAAGAACGGATTCATNTCTTA

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- 128. Staphylococcus caseolyticus (SEQ ID NO. 128) SCAS

 CCGCACATCCCTGTCCATTTACCTTCTTTATGACTGGCATCAATAACTTGTTTGATCAGTCTAAGAATC

 GCTGGGTTATAGGGCTGGTAAAGATAAGAGACGCGTTCACTCATACGGTCTGCAGCCATCGTATATTGA

 ATAAGATCATTCGTACCGATACTAAAGAAATCAACCTCTTTCGCAAAGATATCGGCCATTGCTGCTGTA

 GAAGGAATCTCTACCATGATGCCAAGCTCGATATCGTCAGCAACTTTAACTTTATCTGCAATTAAATTG

 GCTTTCTCTTCTTCTAAGATTGCTTTCGCATCACGGAATTCGTTGATAGTCGCAATCATTGGGAACATG

 ATGCTCAGTTTACCGTGGATGGATGCACGTAATAACGCACGAAGCTGTGTTCTAAAGATATCCTGCTGA

 TCCAGACAAAGTCGAATCGCACGGTATCCAAAGAACGGATTCA

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TCGATCTCTTTGCGCAGTGCACGCACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAA GCCGAGGCACGCAGGATAGCGCGGAGCTGATCGCGCAGGATCTCTTTACGATCCATTGCGATACGGATAGCGCGC CAGCCAAAGAACGGGTTCATTTCTTA

- TCCCGCCATTTCTCCGCACATGCTCACTGGCTTGCCTTCACCATGGGCATCGCGCACCACCGTGCTCAAGGCTTG
 CAGCTCCGCCGGGTGCAGGTAGTCGTACAGGTCGGCAACCCGCGGGTTGTTGCGGTCCACCGCCAGCAGGTACTG
 GGTCAGGTCGTTGGAGCCGACCGACAGGAAATCCACCTGCCGCGCCAGTTCCTTGGTCTGGTACACCGCCGCAGG
 TATTTCCACCATCACGCCCACCGGCGGCATCGGCACATCGGTGCCTTCGTCACGCACCTCGCCCCAGGCGGGTG
 GATCAGGTGCAGCGCTTCTTCCAGCTCGTGGATGCCGGAAATCATCGGCAGCAGGATGCGCAGGTTGTTCAGGCC
 CTCGCTGGCCTTGAGCATGGCGCGAGTCTGCACCAGGAAGATTTCCGGGTGGTCGAGGGTGACGCGGATGCCGCG
 CCAGCCTAAGAATGGATTCATCTCGT

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137. Listeria innocua (SEQ ID NO. 137) LINN

138. Serratia marcescens (SEQ ID NO. 138) SMAR

139. Salmonella enterica hadar (SEQ ID NO. 139) SHAD

140. Salmonella enteritidis (SEQ ID NO. 140) SENT

141. Salmonella enterica Brandenburg (SEQ ID NO. 141) SBRA

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ACGCCAATCTCAATGCTTTCGTCAAATGCTTTACCTTCGTCACGCAGTTCCTGTTTGTAGATTTCAATCTCTTTG
CGCAGCGCGCAACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAAGCGGAGGCACGC
AGAATCGCGCGAACCTGGTCACGCAGGATCTCTTTGCGATCCATGGCGATACGCACGGCGCGCCCAGCCNAAGAAC
GGAT

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146. Streptococcus suis (SEQ ID NO. 146) SSUI

GCCCACATACCAGCCCATTTACCTTCTGCGTGTGCAGCCTTGATAACATTGTTAATCAAGCGAAGGATTGATGGG
TTATATGGTTGGTAGAGGTATGAAACTTGTTCATTCATACGGTCTGCAGCCATTGTGTACTGGATAAGGTCGTTC
GTACCGATTGAGAAGAAGTCAACTTCTTTGGCAAAATTGGTCTGCAAGCATTGCTGCTGCAGGGATTTCAATCATG
ATACCAACTTGGATATCATCCGCAACTGCTACACCTTCAGCCAACAAGTTTGCTTTTTCTTCATCAAGGATTGCT
TTTGCTGCACGGAATTCAGTCAACAAGGCAACCATTGGGAACATGATACGAAGTTTACCATGTACTGATGAACGA
AGAAGGGCACGCAACTGAGTGCGGAACATTTGGTTACCAGTCTCAGAGATAACGAAGGCACGGAAACCN
AAGAA

147. Bacillus pseudomycoïdes (SEQ ID NO. 147) BPMS

148. Staphylococcus lugdunensis (SEQ ID NO. 148) SLUG

CCGCACATACCAGTCCATTTACCTTCTTTATGAGAAGCTTCAATCACTTGTTTCACTAGACGTAAAATAGCTGGA
TTATATGGTTGATAAAGGTATGATACACGTTCTGACATGCGGTCAGCAGCCATTGTGTATTGAATCAAATCATTA
GTACCGATACTGAAGAAATCAACTTCTTTAGCAAAGATATCAGCTAATGCAGCTGTTGATGGGATTTCTACCATT
ATTCCGAGCTCGATATCATCTGACACGTCATGTCCTTCATTTTTTAGATTTTCTTTTTTCTTCTAAAAGAAGCGCT
TTGGCATCTCTAAACTCATTAATAGTAGCAACCATTGGGAACATAATATTTAATTTTTCCATATGCTGAAGCACG
CAAAAGAGCGCGCAACTGTGGTCTGAAAATATCAGGTTGATCTAAGCACAATCGAATCGCACGGTAACCNAAGAA

149. Cryptococcus neoformans (SEQ ID NO. 149) CNEO

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Figure 6. Molecular marker III (SpyM_0902 &SpyM_0903) sequences amplified from Gram positive bacteria (SEQ ID NOs 150-180).

- 151. Enterococus villorum (SEQ ID NO. 151) SVIL

 CCGAAGGGGCAAGGGATAAGACCCGAAACTCTCAGGTAAAAGGACAGAAAGCATTGAATGTTTTTAACTTTCAGT

 AATAGCTTTGTACTTTCAGAGGTCTGGTTAAGCCAAACCTCTTTTTTGATGTCTCGGTCTAAGGAGATTTTAAACG

 CATGTTAGACTTTTCACTTCCATTGATGACTTTGTATGGGGACCTCCCCTTCTTGTCCTTCTTGTAGGAACTGG

 TATCTACCTTACAATCCGTCTTGGACTTTTGCAAATCATTCGTCTGCCTAAAGCCTTTAAACTTATCTTTGCTGA

 AGATAAAGGAGAGGGTGATATTTCTAGTTTTGCAGCCCTTGCCACAGCACTTGCTGCAACTGTTGGTACTGGTAA

 CATTGTTGGTGTTGCGACAGCCATTAAGACTGGTGGGCCTTGTCTTTTCTGGATGTGGATTGCTGCTTTCTT

 TGGAATG

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154. Streptococcus agalactiae (SEQ ID NO. 154) SAGA

158. Staphylococcus simulans (SEQ ID NO. 158) SSIM ATCCGGCTTTGAGTTTAAAGCTATTGATGCTTTAATTACGAACTTCCATCTGCCGAAGTCCACACTTGTCATGTT AGTTTCAGCATTCAGAAACAATATATTTTAAATGCATACCAAACAGCTGTCGAAATGAAATATCGATTCTT CAGCTTTGGTGATGCAATGTTAATTATTTAAGGGAGTCGTGAAAAAGTTATGCCTGCAGTAACTTATGAACATAT

CAAAACATGTAAACAATCCGGTGCAAGGTTAGGAATCGTGCATACACCGCACGGTTCGTTTGAAACACCTATGTT

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TATGCCAGTAGGAACTCAAGCTACCGTTAAAACTATGAGTCCTGAAGAACTAAGGGAAATTAATGCACAAATCAT
TTTAGGCAACACATACCATTTATGGTTGCAACCCGGCAATGACATTATTAAACGCGCGGGTGGTTTGCATAAATT
TATGATTTGGAATGGCCAC

- 160. Streptococus pneumoniae (SEQ ID NO. 160) SPNE
 GTAAAGGCACCGAAGGGGCAAGGCAGGCAACTGCTCAAACTCTCAGGTAAAAGGACAGAGCTAGGATAGACCGCT
 TTTTAGCATTTATCTAAGCATTCCAGAGTACATGTATCTTGCATGTGCTCTTTTCTTTTGGGGTTGAAACGATAGG
 AGAAGGAAATGTTAGAATTGCTTAAATCAATCGATGCTTTTGCTTGGGGACCGCCCCTCTTGATTTTATTGGTCG
 GAACAGGGATTTACCTAACCATGCGGCTAGGACTCTTGCAGGTTTTGCGTCTCCCCAAGGCCTTTCAGCTTATTT
 TTATCCAGGATAAGGGACATGGTGATGTATCCAGTTTTACAGCTCTGTGTACAGCCTTGGCATCAACTGTTGGAA
 CAGGAAATATCATAGGAGTTGCGACGGCTATCAAGGTTGGTGGACCAGGAGCTCTATTTTGGATGTGGATGGCGG
 TTTTCTTTGGAATGGCCC

162. Bacillus anthracis 1978 (SEQ ID NO. 162)

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163. Bacillus anthracis Sterne (SEQ ID NO. 163)

164. Bacillus anthracis Butare (SEQ ID NO. 164)

165. Bacillus anthracis 1655H85 (SEQ ID NO. 165)

166. Bacillus anthracis Coda-Cerva (SEQ ID NO. 166)

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167. Bacillus anthracis 2054H82 (SEQ ID NO. 167)

168. Bacillus cereus ATCC 10987 (SEQ ID NO. 168) BCER10987

169. Bacillus cereus ATCC 14579 (SEQ ID NO. 169) BCER14579

170. Bacillus thuringiensis serovar israelensis BTHUISR (SEQ ID NO. 170)

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171. Bacillus mycoïdes serovar MYC003 (SEQ ID NO. 171) BMYC003

172. Bacillus mycoïdes serovar NRS306 (SEQ ID NO. 172) BMYC306

173. Bacillus thuringiensis serovar Kurstaki BTHUKUR (SEQ ID NO. 173)

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174. Enterococcus faecium (SEQ ID NO. 174) FCM

175. Enterococcus casseliflavus (SEQ ID NO. 175) ECAS

176. Enterococcus flavescens (SEQ ID NO. 176) EFLA

177. Enterococcus gallinarum (SEQ ID NO. 177) EGAL

GAACGGAATTCTGGAGAGACCGTAAAGGCACCGAAGGGGCAAGGCAGGTAACTGCTCAAACTCTCAGGTAAAAGG
ACAGAGCTAGGATAGACCGCTTTTTGGCATTTATCTAAGCATTCCAGAGTACATGTATCTTGCATGTACTCTTTC
TTTTGGGGTTGAAAGATAGGAGAAGGACATGTTAGAATTGCTTAAAGCGCTTGATGCTTTTGCTTGGGGGCCTCC
CCTCTTGATCTTATTGGTCGGAACGGGTATCTATTTGACCATCCGACTGGGCCTTTTGCAGGTTACTCGTCTCCC
TAAGGCCTTTCAGTTGATCTTTACCAAGGACAAGGGGCACGGCGATGTGTCGAGCTTTGCTGCTCTCTGTACGGC
TCTAGCAGCCACAGTTGGTACGGGAAATATCATCGGGGTAGCGACAGCCATTAAGGTTGGAGGACCAGGGGCCCT
CTTTTGGATGTGGATGGCGGCCTTCTTTGGAATGGCAACTAAATACGC

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178. Enterococcus raffinosus (SEQ ID NO. 178) ERAF

GACGGAATTCTGGAGAGACCGTAAAGGCACCGAAGGGGCAAGGCAGGTAACTGCTCAAACTCTCAGGTAAAAGGA
CAGAGCTAGGATAGACCGCTTTTTGGCATTTATCTAAGCATTCCAGAGTACATGTATCTTGCATGTACTCTTTCT
TTTGGGGTTGAAAGATAGGAGAAGGACATGTTAGAATTGCTTAAAGCGCTTGATGCTTTTGCTTGGGGGCCTCCC
CTCTTGATCTTATTGGTCGGAACGGGTATCTATTTGACCATCCGACTGGGCCTTTTGCAGGTTACTCGTCTCCCT
AAGGCCTTTCAGTTGATCTTTACCAAGGACAAGGGGCACGGCGATGTGTCGAGCTTTGCTGCTCTCTGTACGGCT
CTAGCAGCCACAGTTGGTACGGGAAATATCATCGGGGTAGCGACAGCCATTAAGGTTGGAGGACCAGGGGCCCTC
TTTTGGATGTGGATGGCGGCCTTCTTTGGAATGGCCACCAAATACGC

179. Streptococcus mitis (SEQ ID NO. 179) SMIT

180. Streptococcus canis (SEQ ID NO. 180) SCAN

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Figure 7: Molecular marker IV (putative GTP-binding factor plus 160 nt downstream this ORF) sequences amplified from Gram-positive bacteria (SEO ID NOs 181-193)

181. Listeria monocytogenes (SEQ ID NO. 181)

GTTAGAAAAAGGAAGTTCTATTGTAGCATCGCCAAAAATCCATCAAACCTTATTAGATAACTACCTGCCTTAAAG AAAGCGCTCAACATAAAAAAACTTGTTTTCAGAAAATAAAAATCGTGCCAAATCGGCTCAGCTATGCTATAATAG CGATAAATGTTTGGATTTTTAATTTAGGAGGAAACAAGATTGAATTTAAGAAATGATATTCGTAATGTAGCAATT ATTGCCCACGTTGACCATGGTAAAACAACTCTAGTAGACCAATTATTACGCCAGTCAGGCACATTCCGCGACAAT GAAACAGTTGCAGAACGCGCAATGGACAACAATGATTTAGAAAGAGAACGCGGTATTACAATTTTAGCGAAAAAT ACAGCGATTAAGTATGAAGATACACGTGTAAACATCATGGATACACCTGGACACGCCGATTTCGGTGGAGAAGTA GAACGTATCATGAAAATGGTTGATGGTGTTCTTTTAGTAGTGGACGCGTATGAAGGTACGATGCCTCAAACACGT TTTGTACTAAAAAAAGCACTAGAACAAAACCTAACTCCAATCGTAGTAAACAAAATTGACCGTGACTTTGCT CGCCCAGAAGAAGTTGTTGATGAAGTATTAGAATTATTCATCGAACTAGGCGCAAACGACGATCAATTAGAATTC AAACCACTTTTAGACACAATTATCGAACATATCCCGGCTCCAGTTGATAATAGCGACGAACCATTACAATTCCAA GTATCATTACTTGATTATAATGACTATGTTGGTCGTATCGGTATTGGCCGCGTATTCCGTGGAACAATGCACGTG GGACAAACAGTTGCTTTAATTAAACTTGATGGCACAGTAAAACAATTCCGTGTAACGAAAATGTTCGGTTTCTTC GGACTAAAACGTGACGAAATTAAAGAAGCAAAAGCTGGTGATTTAGTAGCATTAGCAGGTATGGAAGACATCTTC GTTGGTGAAACAGTAACACCATTTGACCACCAAGAAGCACTTCCGTTATTACGTATTGATGAGCCAACCTTGCAA ATGACTTTCGTAACAATAACAGTCCTTTCGCTGGTCGTGAAGGTAAACACGTAACAAGCCGTAAAATTGAAGAA $\tt CGTTTACTTGCAGAGCTTCAAACGGACGTATCTTTACGCGTAGAGCCAACAGCTTCCCCTGACGCTTGGGTAGTT$ TCTGGTCGTGGTGAGCTTCATTTATCCATTTTGATCGAAACAATGCGTCGCGAAGGTTATGAATTACAAGTTTCT AAACCAGAAGTAATCATCCGTGAAATTGATGGCGTGAAATGTGAACCAGTAGAAGATGTTCAAATTGATACTCCA GAAGAATTCATGGGTTCCGTTATTGAATCTATCAGCCAACGTAAAGGCGAAATGAAAAACATGATTAACGATGGC AACGGACAAGTTCGTTTACAATTCATGGTTCCAGCTCGTGGCTTAATCGGTTATACAACTGATTTCCTTTCAATG ACTCGTGGTTATGGTATTATCAACCACACA

182. Listeria innocua (SEQ ID NO. 182)

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GATTATAATGACTATGTTGGTCGTATTGGTATTGGCCGCGTTTTCCGTGGAACAATGCACGTAGGACAAACAGTT
GCCTTAATTAAACTAGACGGCACAGTAAAACAATTCCGTGTAACGAAAATGTTCGGTTTCTTCGGACTAAAACGT
GACGAAATTAAAGAAGCAAAAGCGGGTGACTTAGTAGCACTTGCAGGAATGGAAGACATCTTCGTCGGTGAAACA
GTAACACCATTTGACCACCAAGAAGCACTTCCACTTTTACGTATTGATGAGCCAACCTTGCAAATGACTTTTGTA
ACAAATAACAGTCCTTTCGCAGGCCGTGAAGGTAAAACACGTAACAAGCCGTAAAATTGAAGAACGCTTACTTGCA
GAACTTCAAACGGATGTATCTTTACGCGTTGAACCAACAGCTTCTCCAGACGCATGGGTAGTATCTGGTCGTGGT
GAGCTTCACTTGTCTATCTTAATTGAAACGATGCGTCGTGAAGGTTATGAGTTACAAGTTTCTAAACCAGAAGTA
ATCATCCGTGAAATCGATGGCGTGAAATGTGAACCAGTAGAAGACGTTCAAATTGATACTCCAGAAGAATTCATG
GGTTCAGTTATTGAATCTATCAGCCAACGTAAAGGCGAAATGAAAAACATGATTAACGACGGCAATGGCCAAGTT
CGTTTACAATTCATGGTTCCAGCTCGTGGATTAATCGGTTATACAACTGATTTCCTTTCAATGACACGTGGTTAT
GGTATTATCAACCATACATTCGATAGCTACCAACCAATCCAAAAA

183. Bacillus cereus (SEQ ID NO. 183)

TTACTTTCACAAAAGTAAGAATACAACTATATTTTCATTCTTGCTTTTATTTTAATTGCTATTGTATCCCCTTCG CTCTTATAATAGAGAAGGATTAAAAAGACATTAGGAGTTGGACATGTTGAAAAAAACGACAAGATTTACGTAATAT AGCAATTATTGCCCACGTTGACCATGGTAAAACAACACTTGTTGACCAGTTATTACGTCAAGCGGGGACTTTCCG TGCGAACGAACACGTTGAAGAACGCGCAATGGATTCAAATGATCTAGAAAGAGAACGCGGTATTACAATTTTAGC GAAAAATACAGCGATTCACTATGAAGATAAAAGAATTAACATTTTAGATACACCTGGTCACGTGACTTCGGTGG AGAAGTAGAACGTATCATGAAAATGGTTGATGGTGTTTTACTTGTTGTTGATGCATATGAAGGTTGTATGCCACA AACACGATTTGTTTTAAAGAAAGCTCTTGAGCAAAACTTAACTCCAATCGTAGTTGTAAACAAAATTGACCGTGA CTTCGCTCGTCCAGATGAAGTAGTTGATGAAGTAATCGACTTATTCATTGAGCTTGGTGCAAACGAAGATCAATT AGAGTTCCCAGTTGTATTTGCATCAGCAATGAACGGAACAGCAAGCTTAGATTCAAATCCAGCAAATCAAGAAGA GAATATGAAATCATTATTCGATACAATTATCGAACATATTCCAGCACCAATTGATAACAGCGAAGAGCCACTTCA ATTCCAAGTAGCACTTCTTGATTACAACGACTACGTTGGACGTATTGGAGTTGGTCGCGTATTCCGCGGTACAAT GAAGGTTGGACAACAAGTTGCTTTAATGAAAGTAGACGGAAGCGTGAAGCAATTCCGCGTAACGAAATTATTCGG TTACATGGGATTAAAACGTCAAGAAATTGAAGAAGCAAAAGCAGGGGACTTAGTAGCCGTTTCTGGTATGGAAGA CATTAACGTAGGTGAAACAGTATGTCCAGTTGAACATCAAGATGCGTTACCATTATTACGTATTGATGAGCCAAC ACTACAAATGACGTTCCTTGTAAATAACAGCCCATTTGCAGGTCGTGAAGGTAAATACATTACATCTCGTAAAAT TGAAGAGCGTCTTCGTTCACAATTAGAAACAGATGTAAGTTTACGTGTAGATAATACAGATTCTCCTGATGCGTG GATCGTATCTGGACGTGGGGAACTACATTTATCTATCTTAATTGAAAACATGCGTCGTGAAGGTTATGAATTACA AGTATCTAAGCCAGAAGTAATCATTAAAGAAGTTGATGGCGTAAGATGTGAGCCTGTAGAGCGCGTACAAATCGA TGTACCTGAAGAATACACTGGTTCTATTAT

184. Bacillus anthracis (SEQ ID NO. 184)

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TTGAGCAAAACTTAACTCCAATCGTAGTTGTAAATAAAATTGACCGTGACTTCGCTCGTCCTGATGAAGTAGTTG ATGAAGTAATCGACTTATTCATCGAACTTGGTGCAAACGAAGATCAATTAGAGTTCCCAGTTGTATTTGCATCAG CAATGAACGGAACAGCAAGCTTAGATTCAAACCCAGCAAATCAAGAAGAGAATATGAAATCATTATTTGATACAA TTATTGAACATATTCCTGCACCAATTGATAACAGCGAAGAGCCACTTCAATTCCAAGTAGCACTTCTTGATTACA ACGACTATGTTGGACGTATCGGGGTTGGACGCGTATTCCGCGGTACAATGAAGGTTGGACAACAAGTTGCTTTAA TGAAAGTAGACGGAAGTGTAAAACAATTCCGCGTAACGAAACTATTTGGTTATATGGGATTAAAACGTCAAGAAA TTGAAGAAGCAAAAGCTGGAGACTTAGTAGCTGTTTCTGGTATGGAAGACATTAACGTAGGTGAAACAGTATGTC CAGTTGAACATCAAGATGCGTTACCATTATTACGTATTGATGAGCCAACACTACAAATGACATTCCTTGTAAATA AAACAGATGTAAGTTTACGCGTAGATAATACAGAATCTCCTGATGCGTGGATCGTATCTGGACGTGGGGAACTAC ATTTATCTATCTTAATCGAAAACATGCGTCGTGAAGGTTATGAACTACAAGTATCTAAACCAGAAGTAATCATTA AAGAAGTTGATGGCGTAAGATGTGAGCCTGTAGAGCGTGTGCAAATTGATGTACCTGAAGAATACACTGGTTCTA TTATGGAATCTATGGGTGCACGTAAAGGTGAAATGTTAGATATGGTGAATAACGGAAACGGTCAAGTTCGCCTTA CTTTCATGGTTCCAGCACGTGGTTTAATTGGTTACACAACAGAATTCTTAACATTAACTCGTGGTTACGGTATTT TAAACCATACATTCGATTGCTACCAACCAGTACACGCTGGACAAGTTGGTGGACGTCGTCAAGGTGTTCTAGTTT CACTTGAAACAGGAAAAGCATCACAATACGGTATTATGCAAGTTGAAGACCGTGGTGTAATCTTCGTTGAACCAG GTACAGAAGTATATGCTGGTATGA TTGTTG

185. Staphylococcus aureus (SEQ ID NO. 185)

GACTAATAAAAGAGAAGATGTCCGCAATATAGCAATTATTGCTCACGTTGACCATGGTAAAACAACTTTAGTAGA TGAGTTGTTAAAACAATCTGGTATATTCAGAGAAAATGAACATGTCGATGAACGTGCAATGGACTCTAACGATAT CGAAAGAGCGTGGAATTACGATTCTAGCCAAAAATACGGCTGTTGATTAAAGGTACACGTATTAATATTTT GGATACACCAGGACATGCAGACTTTGGTGGAGAAGTAGAACGTATTATGAAAATGGTTGATGGGGTTGTCTTAGT AGTAGATGCGTATGAAGGTACAATGCCTCAAACACGTTTTGTACTTAAAAAAAGCGCTAGAACAAAACCTGAAACC TGTTGTTGTTGATAAAAATTGATAAACCATCAGCACGTCCAGAGGGTGTTGTAGATGAAGTTTTAGATTTATT TATTGAATTAGAAGCAAACGATGAACAATTAGAATTCCCTGTTGTTTATGCTTCAGCAGTAAATGGAACAGCTAG CTTAGATCCTGAAAAACAAGATGATAATTTACAATCATTATATGAAACAATTATTGATTATGTACCAGCTCCAAT TGATAACAGTGATGAGCCATTACAATTCCAAGTAGCATTGTTGGACTACAATGATTATGTTGGACGTATTGGTAT TGGTCGTGTATTCAGAGGTAAAATGCGTGTCGGAGATAATGTATCACTAATTAAATTAGACGGTACAGTGAAAAA CTTCCGTGTAACTAAAATCTTTGGTTACTTTGGATTAAAACGTTTAGAAATTGAAGAAGCACAAGCTGGAGATTT AATTGCTGTTTCAGGTATGGAAGACATTAATGTTGGTGAAACTGTAACACCACATGACCATCAAGAAGCATTGCC AGTTCTACGTATTGATGAGCCTACTCTTGAAATGACATTTAAAGTTAACAATTCTCCATTTGCTGGCCGTGAAGG TGACTTTGTAACAGCACGTCAAATTCAAGAACGTTTAAATCAACAATTAGAAACAGATGTATCTTTGAAAGTTTC TAACACAGATTCTCCAGATACATGGGTAGTTGCTGGTCGCGGTGAATTGCATTTATCAATCCTTATTGAAAATAT GCGTCGTGAAGGTTATGAATTACAAGTTTCAAAACCACAAGTAATTATTAAAGAAATAGATGGTGTAATG

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186. Staphylococcus epidermidis (SEQ ID NO. 186)

AAGAAAGGAATTTATAAAATGACTAATTTAAGAGAAGATGTTCGTAATATAGCGATTATTGCGCATGTCGACCAT GGTAAAACAACATTAGTAGACCAGTTGCTTAAACAATCAGGTATATTTCGTGAAAACGAACATGTCGACGAGCGT GCAATGGACTCTAATGATTTAGAAAGAGAACGTGGTATTACGATTCTTGCTAAGAATACAGCGATAGATTATAAA GGAACGCGTATCAATATATTAGACACACCTGGCCACGCCGATTTTGGTGGTGAAGTTGAACGTATCATGAAAATG GTTGACGGTGTCGTACTAGTGGTTGACGCATATGAAGGTACAATGCCTCAAACTCGTTTTGTTCTTAAAAAAGCT TTAGAACAAAACTTAAAACCGGTTGTAGTTGTGAATAAAATTGATAAACCAGCTGCTAGACCTGAGGGAGTTGTA GATGAAGTATTAGACTTATTCATTGAATTGGAAGCGAATGATGAGCAATTAGACTTCCCAGTTGTTTATGCTTCA GCTGTGAATGGAACAGCAAGTTTAGACTCTGAAAAGCAAGACGAAAATATGCAATCCCTATACGAGACGATTATT GACTATGTACCGGCACCAGTAGATAATTCAGATGAACCATTACAATTCCAAATTGCTTTACTAGATTATAATGAT TATGTAGGTCGTATAGGCGTTGGACGTGTTCAGAGGTAAAATGCGTGTAGGTGATAATGTATCACTAATTAAA TTAGATGGTACAGTTAAGAACTTTCGTGTGACGAAAATATTTGGTTACTTTGGTCTTAAACGTGAAGAAATTGAA GAAGCACAAGCAGGAGACTTAATAGCTGTTTCAGGTATGGAAGATATTAACGTTGGTGAAACAGTTACACCACAT GATGTTTCTTTAAAAGTTACACCTACTGATCAACCAGATTCATGGGTTGTTGCTGGTCGTGGTGAACTACACTTG TCTATTCTTATTGAAAACATGAGACGTGAAGGCTTTGAATTACAGGTTTCTAAACCTCAAGTTATTTTAAGAGAA ATCGATGGTGTTAAGTGAACCATTTGAGCGTGTACAATGTGAA

187. Bacillus subtilis (SEQ ID NO. 187)

TGAAACTTCGAAATGATCTTCGCAACATCGCGATTATTGCCCACGTTGACCATGGGAAAACGACTCTAGTCGATC AGCTTTTACATCAGGCTGGTACGTTCCGTGCCAACGAACAGGTTGCTGAACGCGCAATGGACTCTAATGATCTTG AACGCGAACGCGGCATTACAATATTGGCGAAAAATACTGCGATTAACTATAAAGATACACGTATCAATATTTTGG ACACCCCTGGACATGCAGACTTTGGGGGAGAAGTAGAACGGATTATGAAAATGGTTGACGGCGTAGTGCTTGTCG TTGACGCATATGAAGGCTGTATGCCTCAAACTCGTTTTGTTCTGAAAAAAGCTCTTGAGCAAAACCTGAACCCTG TTGTTGTTGTAAACAAATTGACCGTGACTTTGCTCCTCCAGAGGAAGTTATCGATGAAGTTCTGGATCTGTTCA TTGAGCTTGATGCCAATGAAGAGCAGCTCGAGTTCCCAGTGGTATATGCTTCCGCGATTAATGGAACAGCGAGTC TTGATCCGAAACAGGATGAAAACATGGAAGCTTTATATGAAACCATTATTAAGCATGTTCCGGCACCTGTTG ATAATGCAGAGGAGCCGCTTCAATTCCAAGTTGCCCTTCTTGACTACAACGACTATGTAGGCCGTATCGGAATCG GACGCGTATTCCGCGGCACAATGAAAGTCGGACAGCAGGTTTCTCTTATGAAGCTTGACGGAACGGCAAAGTCAT TCCGTGTTACAAAGATTTTTGGTTTCCAAGGCTTAAAGCGTGTGGAAATTGAAGAAGCAAAAGCGGGAGACCTCG TTGCGGTTTCCGGGATGGAAGATATCAACGTTGGTGAAACGGTATGTCCTGTAGACCATCAAGATCCGCTTCCGG TCCTTCGCATTGATGAGCCGACACTTCAAATGACATTTGTCGTGAATAACAGTCCGTTTGCAGGCCGTGAAGGCA AATATGTAACGGCCCGCAAAATCGAAGAGCGTCTTCAATCACAGCTTCAGACGGATGTGAGCTTGCGTGTTGAGC ${\tt CAACAGCTTCTCCTGATGCTTGGGTTGTTTCAGGACGCGGTGAGCTGCACTTGTCAATTTTAATTGAAAATATGC}$ GTCGTGAGGGCTATGAGCTTCAAGTGTCAAAACCTGAAGTTATTATCAAAGAAATCGACGGCGTACGCTGTGAGC CTGTTGAACGTGTGCAAATTGATGTTCCTGAAGAGCATACTGGCT

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188. Streptococcus mutans (SEQ ID NO. 188)

GGAATGGAAAAGTAAAAGAGAAGAATTAGTTCTTTTTTGAGATAATGACAGGGATTAGTATGAGCTGTTGTCTTT TGTTTTTGCAATACTGGTTGATTGAGGACTTATTTTATAAAATTTGGAGATACCAAGACTGCGACTTTGCTATCT TGGTTTTTCTTTTATATTTTAAAACATTTACATATCTCTCCTGAGTTTTTCCCTAATTTTTATGGTATAATAGAT AAGTTGAAATAAATTAATGTAAAATGTAAGAGGAATTATGACAAATTTTAGAGAAGATATTAGAAATGTTGCTAT CATTGCCCACGTTGACCATGGGAAAACAACCCTTGTTGATGAGCTCTTAAAACAATCGCATACACTTGATGAGCA TAAAAAATTAGAAGAACGTGCGATGGACTCTAATGATCTTGAAAAAGAGCGTGGGATTACTATTCTTGCAAAAA TACTGCTGTTGCCTACAATGGTGTACGTATTAACATTATGGACACCAGGACATGCGGATTTTGGTGGAGAAGT AGAGCGTATCATGAAAATGGTTGATGGGGTTGTTCTTGTTGTTGATGCTTATGAAGGTACCATGCCGCAAACACG TTTTGTTTTGAAAAAAGCTTTGGAACAAACCTGGTTCCAATCGTGGTGATAAGATTGACAAGCCATCAGC TCGTCCGGCAGAAGTTGTTGAAGTTCTTGAACTTTTCATTGAACTTGGAGCAGATGATGACCAGTTAGAGTT TCCAGTCGTTTACGCTTCGGCGATTAATGGAACTTCTTCATTATCAGATGAACCAGCGGATCAAGAACATACAAT AGTGTCTCCTTGATTATAACGACTTTGTTGGACGTATCGGTATTGGGCGAGTCTTCCGTGGTTCTGTTAAAGT CGGGGATCAAGTGACACTTTCTAAACTTGATGGTACAACAAAGAATTTTCGTGTTACAAAACTTTTCGGTTTCTT $\tt CGGTTTGGAACGTCGTGAGATTAAGGAAGCTAAGGCTGGCGATTTGATTGCTGTTTCAGGTATGGAAGATATCTT$ TGTTGGTGAAACGATTACACCAACTGATGCTGTAGAACCACTTCCTATTCTTCACATTGATGAGCCAACTCTGCA AATGACCTTTTTAGCTAACAATTCCCCTTTTGCAGGCCGTGAAGGTAAATTTGTAACCTCGCGTAAGGTAGAAGA GCGTTTGTTGGCAGAATTGCAAACAGATGTTTCCCTTCGTGTAGAAGCCACTGACTCACCAGATAAATGGACGGT $\tt TTCAGGTCGTGGGGAGTTACATCTGTCAATCCTTATTGAAACCATGCGCCGTGAAGGATATGAGCTGCAAGTATC$ ${\tt GCGTCCAGAAGTTATTATCAAAGAAATTGATGGCATCAAATGTGAGCCATTTGAACGCGTGCAAATTGACACACC}$ GGAAGAATACCAAGGTGCTGTTATCCAGTCCCTTTCAGAACGTAAAGGTGAAATGCTTGA

189. Streptococcus pneumoniae (SEQ ID NO. 189)

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CAGGCAGAATTGCAAACAGACGTTTCCCTTCGTGTTGACCCAACTGATTCACCAGATAAATGGACTGTTTCAGGA CGTGGAGAATTGCACTTGTCAATCCTTATCGAAACAATGCGTCGTGAGGGCTATGAACT

190. Streptococcus agalactiae (SEQ ID NO. 190)

AATAGGCAGTTAATATGAAAACATTTACACTTGTGTAAATTCTGTTTTTTAAGAAAAATTGTGTTATAATTCATA AGTTAACAGAATTACATTATAAAATAGAGGAAAACATGACAAATTTAAGAACAGATATCCGTAACGTTGCGATCA TTGCCCACGTTGACCACGGTAAAACAACTCTCGTTGATGAATTATTAAAACAATCACATACTCTTGATGAGCGTA AAGAGCTTGAAGAACGTGCAATGGATTCAAATGATATCGAAAAAGAACGTGGTATCACCATTCTTGCAAAAAATA CAGCCGTAGCATACAACGATGTTCGTATCAATATTATGGACACCTGGTCACGCGGACTTTGGTGGTGAAGTTG AGCGTATTATGAAAATGGTTGATGGTGTTTTTAGTCGTTGATGCCTACGAAGGAACAATGCCACAAACACGTT CTGTTGTTTATGCTTCAGCTATCAATGGAACATCTTCAATGTCAGATGATCCTTCAGATCAAGAAAAAACAATGG CACCGATTTTTGATACTATCATTGATCACATTCCAGCCCCCAGTTGACAACTCGGAAGAACCACTTCAATTCCAAG TTTCTCTTCTTGATTACAATGATTTTGTAGGACGTATTGGTATTGGACGTGTTTTCCGCGGGGACTGTCAAAGTTG GAGATCAAGTTACTCTTTCAAAACTTGATGGTACAACTAAAAACTTCCGCGTAACAAAACTTTTTGGTTTCTTTG GACTTGAACGTAAAGAAATCCAAGAGGCTAAAGCGGGTGATTTAATCGCTGTTTCTGGTATGGAAGATATCTTCG TTGGTGAGACAGTAACTCCGACAGATGCTATTGAACCACTACCAGTTTTACGTATTGACGAGCCAACACTTCAAA TGACTTTCTTGGTGAATAATTCACCATTTGCAGGTCGCGAAGGTAAATGGATTACGTCACGTAAGGTTGAAGAAC GTCTTTTAGCAGAATTACAAACAGACGTTTCTTTACGTGTTGACCCAACAGATTCGCCAGATAAATGGACGGTTT CAGGGCGTGGAGAATTACATTTATCTATCCTTATTGAAACAATGCGTCGTGAGGGATATGAACTTCAAGTATCAC GTCCAGAAGTTATCATCAAAGAAATTGATGGTGTTCAATGCGAGCCGTTTGAGCGTGTTCAAATTGATACTCCAG CACGTGGATATGGTATCATGAATCATACTTTTGACCAGTATCTACCGGTTGTTCAAGGAGAAATTGGTGGTCGTC ATCGTGGTGCCTTGGTTTCTATTGAAAATGGTAAAGCAACTACATATTCAATTATGCGTATTGAAGAACGTGGGA CTATCTTTGTAAATCCAGGTATAGAAGTTTATGAAGGAATGATTGTTGGTGAGAATTCTCGTGATAATGACCTCG GAGTCAATATTACAACTGCTAAACAAATGACAAATGTCCGTTCAGCAACTAAAGATCAAA

191. Streptococcus pyogenes (SEQ ID NO. 191)

GTCTTAAAAGACGGTATTGATTATTGGGATGGCAAAGTTAAACAACCACCTAGTTAAGAGTAACGTGGAGTTAA
GGGGAATAAAGGCAGTCACTGTCTCAAAAACCTTAATTCCTTTTTTTGCTGTATCCAGACTTGCTGAAAGTCTGA
AAATATTTACAATTGATTAAAACCAGTTTTTTAAAACATTTTGTGTTATACTTATCTAGTTAAAATATATTTACT
TAGAGGAACAAATGACTAACTTAAGAAACGATATCCGTAACGTAGCGATTATTGCCCACGTTGACCACGGAAAAA
CAACACTTGTAGATGAATTATTAAAACAATCCCATACTCTTGATGAGCGTAAAGAGCCTTCAAGAGCGTGCCATGG
ATTCCAATGACCTTGAAAAAGAACGTGGGATTACAATCCTTGCGAAAAATACGGCAGTAGCCTATAACGATGTTC
GTATTAACATCATGGATACCCCAGGACACGCGGACTTCGGTGGTGAACGTTTCATGAAAAATGGTTGACG
GGGTTGTTCTTGTTGTGGGATGCCTACGAAGGAACAATGCCCCAGACGCGTTTCGTATTGAAAAAAAGCACTTGAGC
AAAACCTTATCCCGATCGTTGTGGTGAACAAGATTGACAAACCTTCAGCTCCAGCAGAAGTTGTAGATGAAG

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192. Enterococcus faecalis (SEQ ID NO. 192)

CATCACGCAACGGAAATCGGACAAGCATGGGCGTGCGTATTAGCGGTTGTGCAGGTTTGGAAATTATTGCT GAAGAATTTGGGTTTAAATACTCTGGTATTACAGGAAAACCATTAACTTTTGCGGGTCGTGAATACTTTATTGCA GCAACTCCTGAAACCTATGATGAAGTATTTACCCGATATTTAAATGAATCGGAATAATCAAAGAAGAGGCGTTGCT GAAAGGTAAGGCTCTTCCTCTTTTAAAAGAGAAAAATTTGTAAAAAAATGTCCTTGTTTTCAGAAAAAGCCGAAT AATTTCTAAAACTTTCATTATTTTTGCAGGCGAAAGCCTTTTTTTAATGAAAAAGTTTGCTATAATAAGCAGTC GGCTTTTATGGACTTAAGTAACATAAGCGTATATAGATAAGGAGCAATTAAATTGAAATACAGAGATGATATTCG TAACGTGGCAATTATCGCCCACGTTGACCATGGTAAAACAACCTTAGTAGATGAACTTTTTAAAACAATCTGACAC TTTAGATGGACACACACAATTACAAGAACGTGCAATGGATTCCAATGCACTTGAAAGTGAACGTGGAATTACTAT CTTAGCAAAAATACAGCCGTAGATTATAACGGTACACGTATCAACATTCTAGATACACCAGGACACGCGGACTT CGGTGGTGAAGTAGAACGTATCATGAAAATGGTAGACGGTGTTGTTTTAGTTGTCGATGCGTATGAAGGAACAAT GCCTCAAACACGTTTCGTATTGAAAAAAGCATTAGAACAAAAAGTAACACCAATCGTGGTTGTTAACAAAATTGA CAAACCTTCTGCTCGTCCTGAACACGTAGTAGATGAAGTTTTAGAGTTATTCATCGAATTAGGTGCAGACGACGA TCAATTAGATTTCCCAGTTGTTTATGCTTCTGCTTTAAACGGAACTTCAAGTGAATCAGATGATCCAGCAGATCA AGAGCCAACAATGGCCCCAATTTTTGATAAAATTATTGAACATGTGCCAGCTCCAGTTGACAATTCAGACGAACC ACTTCAATTCCAAGTCTCATTACTAGACTACAACGATTACGTTGGACGTATTGGGATTGGCCGTGTGTTCCGTGG CACAATGAAAGTCGGCGACCAAGTTGCGTTGATGAAAATTAGATGGCAGCGTGAAAAATTTCCGTGTAACGAAAAT TTTAGGTTTCTTTGGCTTACAACGTGTGGAAATTGATGAAGCAAAAGCGGGCGATTTAATTGCCGTTTCTGGAAT GGAAGACATTTTCGTTGGGGAAACAGTTGTAGATGTTCACAATCAAGAAGCATTACCAATTCTACACATTGATGA GCCAACCTTACAAATGACTTTCTTAGTTAACAATTCTCCATTTGCGGGACGTGAAGGAAAATACATCACCGCTCG TAAAATCGAAGAACGTTTAATGGCTGAGTTACAAACAGACGTATCTTTACGTGTTGATCCAATTGGCCCAGATTC TTGGACTGTATCAGGTCGTGGCGAATTGCATTTATCAATTTTAATTGAAAACATGCGTCGTGAAGGCTATGAATT ACAAGTTTCTCGTCCAGAAGTTATTGAACGTGAAATTGATGGAGTTAAATGTGAACCATTTGAACGTGTTCAAAT TGACACACCTGAAGA

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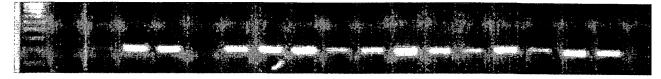
193. Lactococcus lactis (SEQ ID NO. 193)

CGAAAAAGCAAGTTAAATATGTTGTAAATAATGGTGTTACATTAGATAATACTAGTGGTGGGCCTAATTTGGCTG CACCTGTGACGGTGGATAGTCAGGTAATTTCGAACGATAAAGGTACGATTATGGGTGTAAGGACCTATACAGCAG ATTTAAGCCAAGCAGAAGTAGTTAAAAAAGTGGGTAATTTGAATGCAATGTCCTTTGGAGAATTTTGGGGTACAA AAGTTTTTGCTGCCAGCCAAAATCAGACAAATTCAGATAAGACTTATTCTGTTACGTTTAAACTGAATATAAATT GGATAGTATCTAATGGCTATGCTTCGCTAACAAAGTAACAGGTGGCTATGGTTCTTGCATTGACCATGTTTATG TTGCTAATTCTAGTGTTACTCCAACGAATGGTCAGATTAAAGGTTCAAGTGGTTATACTCAACAAGTTGATG ACAAATCAGAAGGGAATAGTTTATCGTGGTCAATTACGCGAAACTATAAACCTGTAAAAGTTCCAGCAAGTGGGG CAAATGTAGGAGCTACGTATTTTGCCACACTTAAACGGGGAAATAGTACATGGAAATTCCAAACAACAAATAGAG CTTATTAAGTGGGAGGAAGTGGAATGAATATAAAAGGCATAAAAATTTGGCAAGTATTTCTTGCATTCATCATTT GGATAGGAACCATGTTTCTTCCTGCAACGGTAAATCAGGCTAAATTGAATACGAATTTTGACTATAAAAAAAGTC GAGAAAATTTCTTTTATTTTCTTTTCATCAAGTCCCTTTTTATAGTTTCATTTTGGGATTGGTGTTGCTTATAT CACTTTTTCTCATTTATAGGAAAATAAATTTTAGTGTCTATTTTTCTTTTGCTAGTCTTATTTTTTACATTAGTT TCTTAGTTATAGCTTTTCCGTCTATGATTATTTTTAATCATAGTTTATCTGGGAATACTTTTTGGGGCTGAACTTT AAGAACTCCTTAGAAATTTTTCTTTGGGGTTTTCATTTTGGAAGTAAAAAAATCTTTGTTAGGCTTGTAAACGTG TGCATTTACAGCTTTTAGAAAAGTGTGCTATAATGGGTTAGATATACGAAAGTAAGGTATGATAAAATTGACT AAATTACGCGAAGATATTAGAAACGTCGCTGTTATTGCCCACGTTGACCATGGTAAAACTACATTGGTTGACGAA CTCTTAAAACAATCTCAAACGTTGGATGCTCGTAAAGAATTAGCTGAACGTGCGATGGACTCAAATGCACTTGAG ${\tt CAAGAACGTGGGATTACTATCCTTGCCAAAAATACAGCAGTTGAATATAACGGAACTCGTATCAACATCTTGGAC}$ A CACCAGGTCACGCGGACTTCGGTGGAGAAGTTGAACGTATTATGAAAATGGTTGATGGGGTTGTCCTCGTTGTCGATGCTTATGAAGGAACAATGCCTCAAACACGTTTTGTTTTGAAA

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Figure 8. Amplification of molecular marker V (carB) in Gram-negative bacteria

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 1



- 1. DNA Ladder (123 bp)
- 2. Pseudomonas aeruginosa
- 3. Pseudomonas pseudoalacaligenes
- 4. Stenotrophomonas maltophilia
- 5. Citrobacter freundii
- 6. Serratia liquefasciens
- 7. Providencia stuartii
- 8. Klebsiella pneumoniae
- 9. Klebsiella oxytoca
- 10.Pseudomonas syringae
- 11. Pseudomonas putida
- 12. Enterobacter aerogenes
- 13. Pseudomonas diminuta
- 14. Proteus mirabilis
- 15. Burkholderia cepacia
- 16.Burkholderia picketti
- 17. Proteus vulgaris
- 18.Serratia marcescens
- 19. Negative control

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Figure 9. Molecular marker V (carB) sequences amplified from different Gram-negative bacteria (SEQ ID NOs 194-232, 238-239, 242-254) and from various Gram-positive bacteria (SEQ ID NOs 233-237, 240-241, 255)

- 195. Neisseria meningitidis groupe C (SEQ ID NO. 195) NMENC
 GTTACCTACATCGAGCCAATTATGTGGCAGACGGTGGAGAAGATTATCGCCAAGGAGCGTCCTGATGCGATTCTG
 CCCACGATGGGCGGTCAGACCGCGCTGAACTGTGCGCTGGATTTGGCGCGCAACGGCGTGCTGGCGAAATACAAT
 GTCGAGCTGATCGGCGGACGGAAGACGCGATTGACAAGGCGGAAGACCGCGGTCGTTTTAAAGAAGCGATGGAA
 AAAATCGGCCTCTCCTGCCCGAAATCTTTTGTCTGCCACACGATGAACGAAGCTTTGGCAGCGCAAGAACAGGTC
 GGCTTCCCTACCCTGATTCGTCCGTCTTTCACGATGGGCGGTTCGGGCGGCGCGCATTGCCTACAATAAAGATGAG
 TTTTTGGCGATTTGCGAACGCGGTTTCGATGCGTCGCCTACGCACGAGCTGCTGATTGAGCAGTCTGTTCCTCGG
 CTGGAAAGA
- 197. Klebsiella pneumoniae (SEQ ID NO. 197) KPNE
 CTACATCGAGCCGATTCACTGGGAAGTGGTGCGTAAAATCATCGAAAAAGAGCGCCCGGATGCGGTGCTGCCGAC
 CATGGGCGGCCAGACGGCGCTGAACTGCGCGCTCGAGCTGGAGCGTCAGGGGGTCCTGGCTGAATTCGGCGTGAC
 CATGATTGGTGCCACCGCCGATGCGATTGATAAAGCCGAAGACCGTCGCCGTTTCGATATCGCAATGAAAAAAAT
 CGGCCTCGACACCGCGGCGCTCTGGTATCGCCCACACGATGGAAGAGGCGCTGGCGGTTGCCGCCGACGTTGGTTT
 CCCGTGCATCATCCGTCCGTCCTTCACCATGGGCGCGCCGCGGCGGCGGTATCGCCTATAACCGCGAAGAGTTCGA

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AGAAATCTGCGAACGGCCTGGATCTCTCCCGACCAACGAACTGCTGATCGATGAATCGCTGATCGGCTGGAA AGA

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207. Salmonella enterica virschow (SEQ ID NO. 207) SVIR

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211. Burkholderia cepacia (SEQ ID NO. 211) BCEP

212. Burkholderia mallei (SEQ ID NO. 212)

GGCGTTGCGTGAGGAGGGCTACAAGGTCATCCTCGTCAACAGCAACCCGGCGACGATCATGACCGATCCGAACAC
GGCGGACGTCACGTACATCGAGCCGATCACGTGGGAAGTCGTCGAGCGCATCATCGCGAAGGAGCGCCCCGACGC
GATCCTGCCGACGATGGGCGGCCAGACCGCGCTGAACTGCGCGCTCGACCTGTTCCACCACGGCGTGCTCGAGAA
GTACGGCGTCGAGCTGATCGGCGCGTCGCCGGAGGCGATCGACAAGGCCGAAGACCGCCAGAAGTTCAAGGACGC
GATGACGAAGATCGGCCTCGGCTGGCGGAAGTCCGGCATCGCGCACTCGATGGAAGAGCGCCTGAAGGTGCACGC
GGACATCGCGGCGGCGACGGGCGAGCGGCTACCCGGTCGTGATCCGCCCGTCGTTCACGCTCGGCGGCTCGGG
CGGCGGCATCGCGTACAACCGCGAGGAGTTCGAGGAGATCTGCAAGCGCGGCCTCGATCTGTCGCCGACGCGCA
GCTGCTGATCGAGGAATCGCTGCTCGGCTGGAAGGAGTACGAGAGTTCGAGGAGGTCGTGCGCCGACCACACTG
CATCATCGTCTGCTCG

213. Burkholderia pseudomallei (SEQ ID NO. 213)

214. Legionella pneumophila (SEQ ID NO. 214)

CGACACTTATGACTGATCCTGAGCTTGCTGATGCCACCTATATAGAGCCTGTTCAATGGAAAGAAGTGGCTCGTA
TTATCGAAATAGAGAGGCCAGATGCTCTTTTACCGACGATGGGAGACAAACAGCCTTAAACTGCGCCTTGGACT
TGGTAAGAGAAGGGGTATTAGCCAAGTACTCTGTTGAAATGATAGGAGCGACGCGTGAAGCCATAGACAGGGCGG
AAGATAGAGAAAAATTTCGCCAGCTGATGATTAAAATCGGATTGGATATGCCAAGGTCGACGATTGCTCATAGCC
TGGAAGAAGCAATTCAAGTACAAGCCCGTTTAGGCTTTCCTGCCATCATCAGGCCTTCATTTACCATGGGTGGTA
GTGGAGGCGGTATTGCCTATAATCGTGAAGAATTTGAAGAAATTTGCATTAGAGGATTGGAGTTGTCGCCAACTC
ACGAGCTTTTGATGATGAATCGGTTCTGGGTTGGAAAGAATATGAAATGGA

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215. Citrobacter freundii (SEQ ID NO. 215)

216. Acinetobacter baumanii (SEQ ID NO. 216) ABAU

217. Serratia marcescens (SEQ ID NO. 217) SMAR

218. Pseudomonas putida (SEQ ID NO. 218) PPUT

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219. Morganella morganii (SEQ ID NO. 219) MMOR

CGAAAAAGAGCGCCCGGATGCCGTTCTGCCGACCATGGGCGGACAAACCGCGCTGAACTGTGCGCTGGATCTGGA
ACGTCACGGCGTGCTGGCAGAGTTCGGCGTCGAAATGATTGGCGCGACAGCAGATGCGATTGATAAAGCCGAAGA
TCGCCGCCGTTTCGATATCGCGATGAAAAAAAATCGGTCTGGATACAGCGCGTTCCGGTATCGCACACCACTGGA
AGAAGCGTTTGCGGTCGCCGATGATGTCGGTTTCCCGTGCATTATCCGCCCGTCATTCACCATGGGCGCACCGG
CGGCGGTATTGCGTATAACCGTGAAGAATTCGAGGAAATCTGTACCCGCGGCCTGGATCTCCCCTGACCAACGA
ACTGCTGATTGATGAATCACTGATTGGCTGGAAAGAGTACGAAATGGAAAGGGCGAATTCCAGCACACTGGCGGC
CGTTACTAGTGGATCA

- 220. Klebsiella oxytoca (SEQ ID NO. 220) KOXY
- CGACAGTTATGACCCGGAAATGGCCGATGCCACCTACATCGAGCCGATTCACTGGGAAGTGGTGCGCAAGA
 TCATTGAGAAAGAGCGTCCGGATGCGGTTCTGCCGACCATGGGCGGCCAGACGGCGCTGAACTGCGCGCTGGAGC
 TGGAGCGTCAGGGCGTGCTGGCCGAGTTCGGCGTGACCATGATTGGCGCGACCGCCGACGCGATTGATAAAGCCG
 AAGACCGCCGCCGTTTCGACGTGGCGATGAAGAAAATCGGTCTCGATACCGCGCGTTCCGGTATCGCGCATACCA
 TGGAAGAAGCGCTGGCGGTTGCCGCTGAAGTTGGCTTCCCGTGCATCATCCGTCCTTTTACGATGGGCGGCA
 CCGGCGGCGGTATCGCCTACAACCGCGAAGAGTTCGAAGAGATCTGCGAACGCGGTCTGGATCTCTCGCCGACCA
 ACGAGCTGCTGATTGATGAATCGCTGATCGGCTGGAAAGAATACGAAATGGAA
- - 222. Brucella melitensis biovar 1 (SEQ ID NO. 222) BMEL1

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223. Brucella melitensis biovar 2 (SEQ ID NO. 223) BMEL2

224. Brucella abortus biovar 1 (SEQ ID NO. 224) BABO1

225. Brucella abortus biovar 2 (SEQ ID NO. 225) BABO2

226. Brucella suis biovar 1 (SEQ ID NO. 226) BSUI1

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CTCGACGTTATAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCAT CGTCGGCAGGATCGCGTCCGGGCGCTCCTTGGCGATGATCTTGGCGACGACTTCCGGCGTGATCGGCTCGATATA GGTTGCATCCGCCAGATCGGGATCAGTATAAA

- CCTCGTGGCGCTTGCGGTCCTCATCCTTGATTTCAGTCGCATTGGCGAGCATCGAGCCCGGCGTGTCGAGGCCGA
 TCTTCTTCATGGCTTCGCGGAAGAGCGCGCGGTCTTCGGCCTTGTCGATAGCTTCGGCCTTGGCGCCGATCATCT
 CGACGTTATAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCATCG
 TCGGCAGGATCGCGTCCGGGCGCTCCTTGGCGATGATCTTGGCGACGACTTCCGGCGTGATCGGCTCGATATAGG
 TTGCATCCGCCAGATCGGGATCAGTATAAATTAGT
 - 228. Brucella canis (SEQ ID NO. 228) BCAN

229. Brucella ovis 69/290 (SEQ ID NO. 229) BOVI

230. Francisella tularensis strain 4/j7 (SEQ ID NO. 230)

CCNACTATTATGACTGATCCANCAACCGCAGATAAAATCTTTATCGAGCCAATTACGGTTGAGAGTGTTGGTAAA ATTATCGCTAGAGAAAAGACCAGATGCAATCTTACCTACAGTAGGTGGACAAACTGCGCTTAACTGTGCTTTAGCA

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TTAGACAAAGCTGGTATTTTAGAAAAATATAATGTCGAAATGCTTGGTGCAAAAGCTGACTCTATTGATAAGGCA
GAAAATAGAGAAAGATTTAACAAAGCCATGGCAAAAATTGGCTTAGAGGTTCCTAGAAATGTTGTAGTGCAATCG
ATGGAGCAAGCTTATAAAGCTCTAGAAGATATCGGACTACCGGCTATTATCAGACCATCATTTACACTTGGTGGT
AGCGGTGGTGGTATCGCTTATACAAAAGAAGAAGATTTGAAAAAATTGTCAAAAATGGTCTAAGCCTATCACCAACA
AATGAAGTACTAATAGAGAGGCCACCCTAANAT

231. Francisella tularensis strain sva/t7 (SEQ ID NO.231)

ACGAANTAGACTGATCCAACAACCGCAGATAAAATCTTTATCGAGCCAATTACGGTTGAGAGTGTTGGTAAAATT
ATCGCTAGAGAAAGACCAGATGCAATCTTACCTACAGTAGGTGGACAAACTGCGCTTAACTGTGCTTTAGCATTA
GACAAAGCTGGTATTTTAGAAAAATATAATGTCGAAATGCTTGGTGCAAAAGCTGACTCTATTGATAAGGCAGAA
AATAGAGAAAAATTTAACAAAGCCATGGCAAAAATTGGCTTAGAGGTTCCTAGAAATGTTGTAGTGCAATCGATG
GAGCAAGCTTATAAAGCTCTAGAAGATATCGGACTACCGGCTATTATCAGACCATCATTTACACTTGGTGGTAGC
GGTGGTGGTATCGCTTATACAAAAGAAGAAGATTTGAAAAAAATTGTCAAAAAATGGTCTAAGCCTATCACCAACAAAT
GAAGTACTAATAGATGAGNCANCCTNAANC

232. Acinetobacter calcoaceticus (SEQ ID NO. 232) ACAL

233. Mycobacterium tuberculosis (SEQ ID NO. 233)

234. Mycobacterium bovis subspecies bovis (SEQ ID NO. 234)

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235. Mycobacterium avium subspecies paratuberculosis (SEQ ID NO. 235)

236. Mycobacterium leprae (SEQ ID NO. 236)

CAAGTGAGTCTGGTCAACTCTAACCCGGCCACCATCATGACCGATCCGGAGTTCGCCGACCACACCTATGTCGAG
CCGATTACGCCGGCCTTCGTGGAGCGGGTGATTGTTCAGCAGGCCGAGCGTGGCAACAGGATTGACGCTTTGCTA
GCCACCTTAGGTGGGCAGACCGCGCTCAACACAGCGGTAGCGCTGTACGAAAACGGAGTGTTGGAGCGCTATGGC
GTCGAGCTCATCGGTGCTGATTTCGAGGCTATCCAGCGTGGTGAGGACCGGCAGCGATTCAAAGATCTCGTCGCT
AAGGTTGGTGGTGAATCCGCTCGCAGTAAAGTGTGTTTCACCATGGATGAGGTGCGTGAAACAGTCGAGGATCTT
GGCCTTCCGGTGGTGGTGCGCCCAAGTTTCACGATGGGCGGATTGGGTTCGGGCATGGCTCACTCCGACGAGGAG
GTTGGCCGGATGGCCGGCCCGGGCTGGTAGCTTCACCTAGTGCCAACGTGCTGATCGAGGAATCGTTTATGGT
TGGAAGGAATTCGAACTCGAGCTAATGCGCGATGGACACCGACAGCGTCGTGGTGGTGCTCCACCACAGAACGTT

237. Nocardia farcinica (SEQ ID NO. 237)

GGTGCTCAAGTCCGAGGGCCTGCGCGTGTCGCTGGTGAACTCGAACCCGGCCACGATCATGACCGATCCCGAGTT
CGCCGACGCCACCTACGTCGAGCCGATCACCCCCGAATTCGTCGAGAAGGTCATCGCCAAGGAGCGCCCCGACGC
GATCCTGGCGACCCTCGGCGGGCAGACCGCGCTCAACACCGCGGTCGCGCTGCACGAGCGCGGCGTGCTGGAGAA
GTACGGCGTCGAACTGATCGGCGCCGACTTCGACGCCATCCAGCGCGGTGAGGACCGGCAGAAGTTCAAGGACAT
CGTCGCCAAGGTCGGCGGTGAGAGCGCCCGCTCGCGGGTCTTCACCATGGACGAGGTCCGCGAGACCGTCGC
CGAACTGGGCTTCCCGGTCGTCGTGCGGCCCTCGTTCACCATGGGCGGCTCGGCTCGGCATGCCTACAACGA
CGAGGACCTGGACCGGATCGCCGGTGGCGGCCTCGCCGACCGCCAACGTCCTGATCGAGGAGTCCAT
CCTCGGCTGGAAGGAATACGAGCTCGAGCTCATGCGCGACGCCGACAACGTCGTGGTGGTCTCCATCGA
GAACGTCGACCCGATGGG

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238. Streptomyces coelicolor (SEQ ID NO. 238)

CCGGCGACGATCATGACCGACCCGGAGATCGCCGACGCCACCTACGTCGAGCCGATCACCCCGAGTTCGTCGAG
AAGATCATCGCCAAGGAGCGCCCCGACGCCCTCCTGCCCACGCTCGGCGGCCAGACGGCCCTGAACACCGCGATC
TCCCTGCACGGCAACGGCGTCCTGGAGAAGTACGGCGTCGAACTGATCGGCGCCAATGTGGAGGCCATCAACAAG
GGCGAGGACCGCGACCTGTTCAAGGAGGTCGTCGAGGAGGTCCGCCAAGAAGATCGGCCACGGCGAGTCCGCCGG
TCCTACATCTGCCACTCCATGGACGACGTCCTCAAGGGCGTCGACGCGCTCGCCGGCGCTACCCCGTCGTCGTCCGC
CCCTCCTTCACCATGGGCGCGCCCGGCTCCGGCTTCGCCCACGACGAGGACGACTGCGCCGGATCGCCGGACAG
GGCCTCACCCTCTCGCCGACCACCGAGGTGCTCCTGGAGGAGGTCCATCCTCGGCTGGAAGGAGTACGAGCTGGAG

239. Streptomyces avermitilis (SEQ ID NO. 239)

240. Corynebacterium efficiens (SEQ ID NO. 240)

241. Corynebacterium glutamicum (SEQ ID NO. 241)

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GAAGAATCCATCCTTGGTTGGAAGGAATTCGAGCTCGAGCTCATGCGCGATACCGCAGACAACGTTGTGGTTATC
TGCTCCATTGAAAACGTCGACGCACTGGGCGTGCAC

242. Bordetella parapertussis (SEQ ID NO. 242)

CCCGCCACCATCATGACCGACCCCGAAACGGCGGACGTCACCTATATCGAGCCCATCACGTGGCAAGCGGTCGAG
AAGATCATCGAGCGCGAGAAGCCCGATGCGCTGCTCCCCACCATGGGTGGCCAGACCGCGCTGAACTGCGCGCTC
GACCTGGCCCACCACGGCGTGCTGAAAAAGCACAACGTCGAGCTGATCGGCGCCAACGAGCACGCCATCGAGAAG
GCCGAAGACCGCCAGAAGTTCAAGCAGGCCATGACCGACATCGGCCTGGAATCGGCCAAGTCGGGCGTGCCCAC
TCGATGGACGAGGCCTGGGAAGTGCAGCGCCGCATCGCGGCCGACATCGGCACGGCGGGCTTTCCCGTCGTCATC
CGCCCCAGCTTCACGCTGGGCGGCTCGGGCGGCGCATCGCCTATAACGCCGAGGAATTCGAGGTCATCTGCCGC
CGCGGCCTGGAAGCCTCGCCGACCAAGGAGCTGCTGATCGAGGAGTTCGAGATG

243. Bordetella bronchiseptica (SEQ ID NO. 243)

244. Bordetella pertussis (SEQ ID NO. 244)

245. Burkholderia mallei (SEQ ID NO. 245)

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GGACATCGCGGCGGCGGCGGCGGCGGCTACCCGGTCGTGATCCGCCCGTCGTTCACGCTCGGCGGCTCGGG CGGCGGCATCGCGTACAACCGCGAGGAGTTCGAGGAGATCTGCAAGCGCGGCCTCGATCTGTCGCCGACGCGCGA GCTGCTGATCGAGGAATCGCTGCTCGGCTGGAAGGAGTACGAGATGGAGGTCGTGCGCGATCGCGCCGACAACTG CATCATCGTCTGCTCG

246. Burkholderia pseudomallei (SEQ ID NO. 246)

GGCGTTGCGTGAGGAGGGCTACAAGGTCATCCTCGTCAACAGCAACCCGGCGACGATCATGACCGATCCGAACAC
GGCGGACGTCACGTACATCGAGCCGATCACGTGGGAAGTCGTCGAGCGCATCATCGCGAAGGAGCGCCCCGACGC
GATCCTGCCGACGATGGGCGGCCAAACCGCGCTGAACTGCGCGCTCGACCTGTTCCACCACGGCGTGCTCGAGAA
GTACGGCGTCGAGCTGATCGGCGCGTCGCCGGAGGCGATCGACAAGGCCGAAGACCGCCAGAAGTTCAAGGACGC
GATGACGAAGATCGGCCTCGGCTGGCGAAGTCCGGCATCGCGCACTCGATGGAAGAGGCGCTGAAGGTGCACGC
GGACATCGCGGCGCGCGCGCGCGCGCGCTCGCCGGTCGTTCACGCTCGGCGGCTCGGG
CGGCGGCATCGCGTACAACCGCGAGGAGTTCGAGGAGATCTGCAAGCGCGGCCTCGATCTGTCGCCGACGCGCA
GCTGCTGATCGAGGAATCGCTGCTCGGCTGGAAGGAGTACGAGATGGAGGTCGTGCGCGACCACACTG
CATCATCGTCTGCTCG

247. Pseudomonas putida (SEQ ID NO. 247)

GCCTGTAAAGCCCTGCGCGAGGAAGGTTTCCGCGTCATCCTGGTGAACTCCAACCCAGCCACCATCATGACCGAC
CCGGCCATGGCTGACGCCACCTACATCGAGCCGATCAAGTGGCAATCGGTGGCCAAGATCATCGAGAAAGAGCGC
CCGGACGCCGTCCTGCCGACCATGGGTGGCCAGACCGCCCTGAACTGCGCCCTGGACCTGGAGCGCCACGGCGTT
CTGGAGAAGTTCGGCGTGGAGATGATCGGTGCCAACGCTGACACCATCGACAAGGCCGAAGACCGTTCGCGCTTC
GACAAGGCCATGAAGGACATCGGCCTGGAGTGCCCGCGCTCCGGTATCGCCCACAGCATGGAAGAGGCCAATGCG
GTCCTCGAGAAGCTCGGCTTCCCGTGCATCATTCGCCCGTCGTTCACCATGGGCGGCACCGGCGGGTATCGCT
TACAACCGTGAAGAATCTGCAACCGTGGTCTGGACCTGTCGCCGACCAAAGAGCTGCTGATCGAC
GAATCGCTGATCGGCTGGAAGAATACGAGATGGAGGTGGTCCGCGACAAGAAGAACTGCATCATCGŢCTGC
TCGATCGAGAACTTCGACCCGATGG

248. Yersinia pseudotuberculosis (SEQ ID NO. 248)

ATGCCAAAACGTACAGATATAAAAAGCATCCTGATTCTGGGCGCAGGCCCGATTGTTATCGGCCAGGCTTGTGAG
TTTGACTACTCCGGTGCCCAAGCGTGTAAAGCACTGCGCGAAGAGGGTTACCGTGTCATTTTGGTGAACTCCAAT
CCGGCGACTATCATGACTGACCCGGAAATGGCCGATGCAACTTATATCGAGCCAATTCATTGGGAAGTGGTGCGT
AAGATTATCGAAAAAGAGCGTCCAGATGCTGTTTTGCCTACGATGGGTGGCCAAACTGCACTGAACTGTGCATTG
GAACTGGAGCGTCAGGGTGTTCTGGCAGAAATTTGGCGTCACCATGATTGGTGCGACCGCCGATGCCATCGATAAA
GCCGAAGACCGCCGTCGCTTTGATATCGCGATGAAGAAGATTGGTCTGGATACGGCCCGCTCAGGTATTGCGCAT
AACATGGAAGAAGCACTGGCTGTTGCCGCTGATGTGGGCTTCCCGTGCATTATCCGCCCATCCTTTACGATGGG
GGCACTGGTGGCGGTATCGCTTATAACCGTGAAGAGTTCGAAGAGATCTGCGAGCGCGGTCTGGATTTGTCACCA
ACCAAAGAGTTGTTGATTGACGAATCGCTGATTGGCTGGAAAGAGTTCACACCGGCGACTCTATCACTGTC
GCACCGGCTCAGACCCTGACCGATAAAGAATCCCAAATCATGCGTAATGCCTCGATGGCGTTACTTGAGATG
GGGGTAGAAACCGGGGGCTCTAACGTACAGTTCTCCGTCAACCCAAAAAATGGTCGTTTGATTGTCATTGAGATG

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AACCCGCGTGTTTCTCGCTCTTCAGCACTGGCCTCTAAAGCAACCGGTTTCCCGATTGCCAAGATTGCCGCCAAA CTGGCGGTCGGTTACACACTGGATGAGTTGATGAATGACATCACCGGTGGCCGTACTCCTGCGTCCTTTGAGCCT TCTATCGACTATGTTGTTACCAAGATCCCACGCTTTAACTTTGAAAAATTTGCGGGTGCCAACGACCGTTTGACC GGGCTGGAAGTGGCCGACCGGTTTTGACCCGAAAGTGAGCCTGGATGATCCCGAAGCACTGACTAAAATTCGT CGTGAATTGAAAGAAGCGGGTGCAGAACGTATCTGGTATATCGCTGATGCTTTCCGTGCGGGCATGTCGGTTGAT GGTGTGTTCAATCTGACCAATGTTGATCGCTGGTTCCTGGTGCAGATTGAAGAGCTGGTTCGTCTGGAAGAGAGC GTGGCAGAACTCGGTATCAACGGCTTGACTGCTGAATTTATGCGTCACTTGAAACGTAAAGGTTTCGCCGATGCT CGTTTGGCTAAATTGGTCGGTGCAGCAGAAAGTGAAGTCCGTAAACTGCGTTACAAATATGGTTTACACCCGGTT TATAAGCGTGTTGATACCTGCGCGGCAGAGTTCTCGACGGATACGGCTTACATGTACTCCACCTACGAGGAAGAG TGCGAATCTAACCCAACCAGCGATCGTCCGAAAGTGATGGTGCTGGGTGGCGGCCCGAACCGTATCGGACAAGGT ATTGAGTTCGACTATTGCTGCGTACACGCTTCATTGGCACTGCGTGAAGACGGTTACGAAACCATCATGGTGAAC GTGTTGGAAATTGTCCGTATTGAGAAACCACAGGGCGTTATCGTGCAGTACGGTGGTCAGACACCGCTGAAATTA GCCCGCGAGTTGGAAGCGGCTGGCGTCCCCATTATTGGGACCAGTCCGGATGCCATTGACCGTGCCGAAGACCGT GCGGTGGAAAAAGCCACTGGTCTGGGCTATCCACTGGTCGTACGCCCTTCTTATGTTTTGGGTGGCCGCGATG GAAATTGTTTATGACGAGATTGACCTGCGCCGTTACTTCCAGAATGCCGTCAGTGTATCGAATGATGCGCCGGTA TTGCTTGACCGCTTCCTTGATGATGCCGTCGAAGTGGATGTCGATGCCATTTGTGATGGTGAACGCGTGTTGATC GGCGGCATTATGGAACATATAGAGCAAGCCGGGGTTCACTCTGGTGACTCAGCCTGTTCATTGCCTGCTTACACC CTGAGCAAAGAAATTCAGGATGTGATGCGCCAACAAGTGGAAAAACTGGCCTTTGAACTCTGTGTCCGCGGCCTG ATGAATGTGCAGTTTGCGGTGAAAAACAACGAAGTTTACCTGATTGAGGTTAACCCACGGGCGGCCCGTACTGTA CCTTTCGTGTCCAAAGCGACCGGTATGCCACTGGCAAAAATTGCCGCTCGTGTGATGGTCGGCCAATCGCTGGCT GAGCAGGCATGCTGGAAGAAATTATTCCGCCTTACTACTCAGTCAAGGAAGTGGTACTGCCGTTTAATAAATTC CCCGGTGTTGACCCAATTTTAGGGCCAGAAATGCGCTCTACCGGTGAAGTCATGGGGGTTGGCCGTACCTTCGCT GAGGGGGATAAGCACCGGGTGGTAGACTTGGCGGCGAAGCTGCTAAAACAAGGCTTTGAACTGGATGCAACCCAC GGAACGGCGTCGTGCTGGCCGAGGCGGGGTAAACCCACGTTTGGTTAACAAGGTGCATGAAGGCCGTCCGCAT ATTCAGGACCGTATTAAGAATGGCGAGTACACCTATATCGTGAATACCACAGCTGGGCGTCAGGCGATTGAAGAT TCTAAGCTGATCCGTCGCAGTGCTTTGCAATATAAAGTGCATTACGATACGACCTTGAACGGTGGTTTTGCTACG AAAGCGTAA

249. Yersinia pestis (SEQ ID NO. 249)

ATGCCAAAACGTACAGATATAAAAAGCATCCTGATTCTGGGCGCAGGCCCGATTGTTATCGGCCAGGCTTGTGAG
TTTGACTACTCCGGTGCCCAAGCGTGTAAAGCACTGCGCGAAGAGGGGTTACCGTGTCATTTTGGTGAACTCCAAT
CTGGCGACTATCATGACTGACCCGGAAATGGCCGATGCAACTTATATCGAGCCAATTCATTGGGAAGTGGTGCGT
AAGATTATCGAAAAAAGAGCGTCCAGATGCTGTTTTTGCCTACGATGGGTGGCCAAACTGCACTGAACTGTGCATTG
GAACTGGAGCGTCAGGGTGTTCTGGCAGAATTTGGCGTCACCATGATTGGTGCGACCGCCGATGCCATCGATAAA
GCCGAAGACCGCCGTCGCTTTGATATCGCGATGAAGAAGATTGGTCTGGATACGGCCCGCTCAGGTATTGCGCAT

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AACATGGAAGAAGCACTGGCTGTTGCCGCTGATGTGGGCTTCCCGTGCATTATCCGCCCCATCCTTTACGATGGGG GGCACTGGTGGCGGTATCGCTTATAACCGTGAAGAGTTCGAAGAGATCTGCGAGCGCGGTCTGGATTTGTCTCCA ACCAAAGAGTTGTTGATTGACGAATCGCTGATTGGCTGGAAAGAGTACGAAGAGTTGTCCGTGATAAAAAC GACAACTGCATCGTTTGCTCCATTGAAAACTTCGATGCGATGGGGATTCACACCGGCGACTCTATCACTGTC GCACCGGCTCAGACCCTGACCGATAAAGAATACCAAATCATGCGTAATGCCTCGATGGCGGTACTGCGTGAAATC GGGGTAGAAACCGGGGGCTCTAACGTACAGTTCTCCGTCAACCCAAAAAATGGTCGTTTGATTGTCATTGAGATG AACCCGCGTGTTTCTCGCTCTTCAGCACTGGCCTCTAAAGCAACCGGTTTCCCGATTGCCAAGATTGCCGCCAAA $\tt CTGGCGGTCGGTTACACACTGGATGAGTTGATGAATGACATCACCGGTGGCCGTACTCCTGCGTCCTTTGAGCCT$ TCTATCGACTATGTTGTTACCAAGATCCCACGCTTTAACTTTGAAAAATTTGCGGGTGCCAACGACCGTTTGACC GGGCTGGAAGTGGGCGCGACCGGTTTTGACCCGAAAGTGAGCCTGGATGATCCCGAAGCACTGACTAAAATTCGT CGTGAACTGAAAGAAGCGGGTGCAGAACGTATCTGGTATATCGCTGATGCTTTCCGTGCGGGCATGTCGGTTGAT GGTGTGTTCAATCTGACCAATGTTGATCGCTGGTTCCTGGTGCAGATTGAAGAGCTGGTTCGTCTGGAAGAGAGC GTGGCAGAACTCGGTATCAACGGCTTGACTGCTGAATTTATGCGTCACTTGAAACGTAAAGGTTTCGCCGATGCT CGTTTGGCTAAATTGGTCGGTGCAGCAGAAAGTGAAGTCCGTAAACTGCGTTACAAATATGGTTTACACCCGGTT TATAAGCGTGTTGATACCTGCGCGGCAGAGTTCTCGACGGATACGGCTTACATGTACTCCACCTACGAGGAAGAG TGCGAATCTAACCCAACCAGCGATCGTCCGAAAGTGATGGTGCTGGGTGGCGGCCCGAACCGTATCGGACAAGGT ATTGAGTTCGACTATTGCTGCGTACACGCTTCATTGGCACTGCGTGAAGACGGTTACGAAACCATCATGGTGAAC TGTAACCCTGAGACGGTTTCAACCGATTATGACACCTCTGATCGTCTCTACTTCGAGTCACGCTGGAAGAT GTGTTGGAAATCGTCCGTATTGAGAAACCACAGGGCGTTATCGTGCAGTACGGTGGTCAGACACCGCTGAAATTA GCCCGCGAGTTGGAAGCGGCTGCCGTTATTGGGACCAGTCCGGATGCCATTGACCGTGCCGAAGACCGT GCGGTGGAAAAAGCCACTGGTCTGGGCTATCCACTGGTCGTACGCCCTTCTTATGTGTTGGGTGGCCGCGCGATG GAAATCGTTTATGACGAGATTGACCTGCGCCGTTACTTCCAGAATGCCGTCAGTGTATCGAATGATGCGCCGGTA TTGCTTGACCGCTTCCTTGATGCCGTCGAAGTGGATGTCGATGCCATTTGTGATGGTGAACGCGTGTTGATC GGCGGCATTATGGAACATATAGAGCAAGCCGGGGTTCACTCTGGTGACTCAGCCTGTTCATTGCCTGCTTACACC CTGAGCAAAGAATTCAGGATGTGATGCGCCAACAAGTGGAAAAACTGGCCTTTGAACTCTGTGTCCGCGGCCTG $\tt ATGAATGTGCAGTTTGCGGTGAAAAACAACGAAGTTTACCTGATTGAGGTTAACCCACGGGCGGCCCGTACTGTA$ $\verb|CCTTTCGTGTCCAAAGCGACCGGTATGCCACTGGCAAAAATTGCCGCTCGTGTGATGGTTGGCCAATCGCTGGCT| \\$ GAGCAGGCATGTTGGAAGAATTATTCCGCCTTACTCAGTCAAAGAAGTGGTACTGCCGTTTAATAAATTC CCCGGTGTTGACCCAATTTTAGGGCCAGAAATGCGCTCTACCGGTGAAGTCATGGGGGTTGGCCGTACCTTCGCT GAGGGGGATAAGCACCGGGTGGTAGACTTGGCGGCGAAGCTGCTAAAACAAGGCTTTGAACTGGATGCAACCCAC GGAACGGCGGTCGTGCTGGGCGAGGCGGGGATAAACCCACGTTTGGTTAACAAGGTGCATGAAGGCCGTCCGCAT ATTCAGGACCGTATTAAGAATGGCGAGTACACCTATATCGTGAATACCACAGCTGGGCGTCAGGCGATTGAAGAT TCTAAGCTGATCCGTCGCAGTGCTTTGCAATATAAAGTGCATTACGATACGACCTTGAACGGTGGTTTTGCTACG GCGATGGCGTTAAATGCGGATCCAACCGATCAAGTGATTTCGGTGCAAGAGATGCCAAGATTAAGAATATG AAAGCGTAA

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250. Vibrio cholerae (SEQ ID NO. 250)

ATGCCAAAACGTACTGACATTCAAAGCATCCTTATCCTTGGTGCGGGTCCAATTGTTATCGGTCAGGCTTGTGAG TTTGACTACTCAGGCGCGCAAGCGTGTAAAGCCCTGCGCGAAGAGGGTTACCGCGTTATTCTGGTTAACTCAAAC CCAGCGACCATCATGACCCAGAAATGGCCGATGCGACTTACATCGAGCCTATCCACTGGGAAGTGGTGCGT AAGATCATCGAAAAAGAGCGCCCAGATGCGATTTTGCCCACCATGGGCGGCCAGACTGCGCTGAACTGTGCGCTG GCACTCGAAAAACATGGCGTATTGGCTGAGTTTGGCGTTGAGATGATCGGCGCAACCGCCGATGCGATTGATAAA AGCATGGAAGAAGCGTACAAAGTCCTCGATATGGTTGGCTTCCCATGTATCATCCGTCCTTCTTTCACCATGGGC GGCAGCGGTGGTGTATCGCTTACAACCGTGAAGAGTTTGAAGAAATCTGTACTCGCGGTCTGGATCTTTCACCG ACCAATGAACTGCTGATCGATGAATCACTGATTGGTTGGAAAGAGTACGAGATGGAAGTGGTGCGTGATAAGAAC GATAACTGCATCATCGTCTGTGCGATTGAAAACTTCGACCCAATGGGCATCCACACGGGTGACTCGATCACTGTC GCTCCAGCGCAAACGCTAACTGACAAAGAATACCAAATCATGCGTAACGCCTCTTTGGCGGTACTGCGTGAAATC GGCGTAGAAACCGGCGGTTCAAACGTTCAGTTTGGTATCAACCCGAAAGATGGCCGCATGGTGATCATCGAGATG AATCCACGTGTATCGCGCTCTTCTGCGTTGGCTTCAAAAGCCACCGGTTTCCCAATTGCGAAAGTGGCGGCCAAA ACCATCGACTACGTGGTCACTAAGATCCCTCGTTTCAACTTCGAAAAATTCGCCGGTGCCAATGACCGTCTGACT ACACAAATGAAGTCAGTAGGTGAGGTGATGGCGATTGGTCGTAACCAACAAGAATCACTGCAAAAAAGCACTGCGC GGCTTGGAAGTGGGTGCGGCTGGTCTGGATGAGAAAGTGGATCTGGACGCCCAGACGCTCTGACCAAAATTCGT TATGAGCTGAAAGAAGCAGGCGCAGAGCGTATTTGGTACATCGCGGATGCATTCCGTGCCGGTATGTCAGTGGAT GGGGTATTTAACCTGACCAACATCGATCGCTGGTTCCTAGTGCAAATTGAAGAACTGGTGAAGCTGGAAGCCGAA GTGAAAGCCGGTGGCTTTGCGGGCTTGAACCAAGACGTACTGCGTAAGATGAAGCGCAAAGGCTTCTCTGATGCG CGTTTGTCAAAACTGCTCGGCGTGAGCGAAAACGAAATCCGTCGTCTGCGTGACCAATACAACATCCACCCAGTT TACAAGCGTGTGGATACCTGCGCGGCAGAATTTAAGTCAGATACGGCTTACATGTACTCCACGTATGATGAAGAG TGTGAAGCCAATCCGACTGACAAAGACAAGATCATGGTGCTGGGCGGTGGTCCAAACCGTATCGGTCAAGGTATC GAGTTTGACTACTGCTGTACACGCCGCGCTTGCACTGCGTGAAGATGGTTACGAAACCATCATGGTTAACTGT AACCCAGAAACCGTATCAACCGATTACGACACCTCAGATCGCCTCTACTTTGAGCCTGTAACTCTAGAGGATGTG CTGGCTATCGTGCGTGTTGAGAAGCCAAAAGGCGTGATCGTGCAGTACGGCGGTCAAACACCACTGAAACTGGCG CGAGCGCTGGAAGCCGCTGGCGTACCTGTGATTGGTACCAGCCCAGATGCGATTGACCGCGCTGAAGACCGTGAA CGTTTCCAACAAGCGGTACAGCGTTTAGGCCTCAAACAGCCAGACAACGCAACCGTAACCGCTATCGAGCAAGCG ATTGAGAAGTCGCGTGAAATCGGTTTCCCACTCGTAGTTCGCCCCTCTTATGTTCTGGGTGGCCGTGCGATGGAG CTGGATCGCTTCCTTGATGATGCAACCGAAGTGGACGTGGATGCGATTTGTGACGGTGAGCGCGTGGTGATTGGC GGCATCATGGAGCACATTGAACAAGCGGGTGTTCACTCAGGTGACTCAGCCTGTTCTCTGCCGGCTTACACCTTG AGCCAAGAAATCCAAGACAAGATGCGTGAGCAAGTTGAGAAGTTGGCATTTGAACTCGGTGTTCGTGGCCTGATG AACATTCAGTTTGCAGTCAAAGACAACGAAGTTTACCTGATTGAAGTAAACCCACGTGCTGCGCGTACTGTGCCG TTTGTTTCTAAAGCAACCGGTGCTCCGCTGGCGAAAATCGCGGCGCGCGTGATGGTTGGACAAACTCTGGAGCAA CAAGGCTTCACCAAAGAGATCATTCCACCTTACTACTCAGTTAAAGAAGTGGTTCTGCCGTTCAACAAGTTCCCG GGGGTTGACCCACTGCTTGGCCCTGAAATGCGCTCAACCGGTGAAGTGATGGGTGTGGGTGCCACGTTTGCTGAA GCCTATGCTAAAGCAGAGTTGGGCTGTGGCTCGGTTTACCCTGAAGGTGGTCGTGCGCTACTTTCGGTGCGTGAA GGTGACAAACAGCGTGTAGTGGATCTGGCTTCTAAGCTAGTGAAACTGGGTTACCAGTTGGATGCGACTCACGGT

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ACTGCAGTGATTCTGGGCGAAGCGGGCATCAACCCACGTCTGGTTAACAAAGTGCATGAAGGTCGTCCACACATT
CTGGATCGCATCAAAAACCACGAGTACACCTACATTGTGAACACGGCTTCTGGCCGCCAAGCAATTGAAGACTCA
AAAGTACTGCGCCGTGGTGCATTGGCTCACAAAGTGAACTACACCACCACCACCTGAACGCCGCCTTCGCAACTTGT
ATGTCACACACGGCGGATGCCAAAGCATCCGTCACTTCAGTACAAGAGCTGCATGCGCGTGTAAAAGCGAACCAA
GCTTAA

251. Vibrio vulnificus (SEQ ID NO. 251)

ATGCCAAAACGTACTGACATTCAAAGCATTCTTATCCTAGGTGCTGGTCCAATTGTTATCGGTCAGGCTTGTGAG TTTGACTACTCAGGCGCACAAGCATGTAAAGCGCTACGTGAAGAAGGTTACCGAGTTATCCTAGTAAACTCGAAC CCAGCGACCATCATGACAGACCCAGATATGGCGGATGCGACCTACATCGAGCCAATTCAATGGGAAGTGGTACGC GCGCTTGAAAAGCACGGCGTGCTAGCGGAATTTGGCGTAGAAATGATCGGTGCAACTGCTGATGCCATCGATAAA GCGGAAGACCGTTCGCGTTTCGACAAAGCGATGAAATCTATCGGCCTAGAGTGTCCTCGTGCTGATACGGCGAAG ACCATGGAAGAGCGTACAAAGTGCTCGATATGGTTGGCTTCCCATGTATCATCCGCCCGTCATTCACCATGGGT GGTACGGGGGGGGTATCGCGTACAACAAAGAAGATTCGAAGAAATCTGTCGCCGTGGTCTTGACCTGTCGCCA ACCAATGAACTGCTTATCGATGAATCTTTGATCGGTTGGAAAGAGTACGAAATGGAAGTGGTTCGCGACAAAGCG GACAACTGTATCATCGTATGTTCAATCGAAAACTTCGACCCAATGGGCATCCACACCGGTGACTCTATCACCGTG GCACCGGCTCAAACGCTGACAGATAAAGAATACCAACTGATGCGTAATGCGTCGCTAGCGGTACTTCGTGAAATC GGTGTAGAGACAGGTGGTTCAAACGTGCAGTTTGGTATCAACCCGAAAGATGGCCGTATGGTTATCATCGAGATG AACCCACGTGTATCGCGCTCTTCTGCTCTAGCGTCAAAAGCGACAGGTTTCCCTATTGCGAAGATTGCAGCGAAA CTAGCCGTTGGCTTCACGCTTGATGAGCTACAAAATGACATCACTGGTGGTGCGACGCCAGCATCATTTGAACCG ACCATCGACTACGTAGTGACTAAGATTCCTCGTTTCAACTTCGAGAAATTTGCCGGTGCTAACGACCGTTTGACG ACGCAAATGAAGTCAGTTGGTGAAGTGATGGCCATTGGCCGTAACCAACAAGAATCACTGCACAAAGCGCTGCGC GGTCTAGAAGTGGGCGCGACTGGTTTTGATGAGATGGTTGATCTTGATTCACCAGATGCACTGACCAAAATTCGC CACGAGCTGAAAGAAGCGGGCGCTGAGCGTATTTGGTACATTGCCGATGCATTCCGTGCGGGTATGTCAGTTGAT GGTGTGTTTAACCTAACTAACATCGATCGCTGGTTCCTGGTTCAAATCGAAGAGATTGTGAAGCTGGAAGAGCAA GTGAAAGCGGGTGGTTTTGCTGGTTTAACTCAAGATGTGCTTCGTCAAATGAAGCGTAAAGGTTTCTCCGACGCT CGCCTATCAAAACTACTCGGCGTGGCTGAAAGTGAAATCCGTCGTCTACGTGACCAATTCGACATCCACCCTGTA TACAAGCGTGTTGATACCTGTGCGGCAGAATTCTCATCGGATACGGCTTACATGTACTCATCTTATGATGATGAG TGTGAAGCGAACCCAACCGATAAAGAAAAGATCATGGTTCTGGGCGGTGGTCCAAACCGTATCGGTCAAGGTATT GAGTTTGACTACTGCTGTTACACGCTTCGCTAGCGCTACGTGAAGATGGTTACGAGACCATCATGGTGAACTGT AACCCAGAAACCGTATCAACCGACTACGACACTTCAGACCGTCTCTACTTTGAACCGGTTACTCTAGAAGATGTG TTGGCGATTGCTCGTGTTGAAAAGCCAAAAGGCGTGATCGTGCAGTACGGTGGTCAAACTCCACTGAAACTGGCG CGTGCGCTAGAAGCGGCGGGTGTACCAATTATCGGTACTAGCCCTGATGCCATCGACCGTGCGGAAGACCGTGAG CGTTTCCAACAAGCGGTTGACCGCTTAGGCCTGCTACAGCCAGAGAACCGTAACCACCATGGAGCAAGCG ${\sf CTGGATCGCTTCCTAGACGATGCAATTGAAGTCGATATCGACGCTATCTGTGACGGTGAGCGCGTGGTGATTGGC}$ AGCCAAGAAATCCAAGACAAGATGCGTGAGCAAGTTGAAAAGCTGGCATTTGAGTTGGGCGTTCGTGGCCTAATG

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AACACGCAGTTTGCCGTAAAAGACAACGAAGTGTACCTCATCGAAGTGAACCCTCGTGCTGCACGTACCGTTCCA
TTCGTATCGAAAGCGACCGGTGCACCACTTGCGAAAATCGCAGCACGTGTTATGGCTGGTCAGTCTCTGGAATCG
CAAGGTTTCACCAAAGAGATTATTCCTCCTTACTACTCGGTAAAAGAAGTGGTTCTGCCATTTAACAAGTTCCCT
GGCGTTGACCCACTATTGGGCCCTGAAATGCGCTCAACGGGTGAAGTGATGGGTGTAGGTGCAACTTTTGCTGAA
GCGTATGCGAAAGCAGAACTGGGTTGTGGCAATGTGTATCCTGAAAGTGGTCGTGCGCTGCTTTCGGTACGCGAA
GGCGACAAGCAACGTGTGGTTGACCTAGCGTCTAAATTACTGAAACTAGGGTACAAGCTGGATGCGACACACGGT
ACGGCAGTGATCTTAGGTGAAGCGGGCATCAACCCACGTCTAGTAAACAAAGTGCACGAAGGTCGTCCTCACATT
CTTGACCGCATCAAGAACAACGAATACACCTACATCGTGAACACGGCGGCTGGTCGTCAAGCGATTGAAGATTCG
AAAGTTCTACGCCGTGGCGCACTTGCAGAAAAAGTGAACTACACCACGACACTTAACGCGGCATTTGCGACCTGT
ATGTCTCATACGGCGGACGCGAAAGCAAGCGTGACGTCGGTACAGGAACTGCACGCGCAAGTGCAAGCGAGTTTG
AAAGCGTAA

252. Vibrio parahaemolyticus (SEQ ID NO. 252)

ATGCCAAAACGTACTGACATTCAAAGTATTCTAATTCTTGGTGCTGGTCCGATTGTTATCGGTCAGGCATGTGAG TTTGACTACTCTGGCGCACAAGCGTGTAAAGCTCTTCGTGAAGAAGGCTACCGAGTTATTCTAGTTAACTCTAAC CCAGCAACCATCATGACAGACCCTGAAATGGCAGATGCAACTTACATCGAGCCGATTCAATGGGAAGTTGTTCGC AAGATCATTGAGAAAGAACGCCCAGATGCAGTATTGCCAACAATGGGTGGTCAGACGGCGCTTAACTGTGCGCTA GATCTAGAGAAGCACGGCGTTCTTGCTGAATTCGGCGTAGAGATGATTGGCGCAACGGCTGACGCGATTGATAAA GCAGAAGACCGTTCTCGCTTCGATAAAGCAATGAAGTCTATCGGCCTTGAGTGTCCTCGTGCTGATACCGCGAAG ACGATGGAAGAAGCTTACAAAGTTTTAGACATGGTTGGCTTCCCTTGTATCATCCGTCCATCGTTCACCATGGGT GGTACGGGTGGCGGTATCGCGTACAACAAAGAAGATTTGAAGAAATCTGTCGTCGTGGTCTGGATCTTTCTCCG ACTAACGAACTTCTTATCGATGAATCGCTAATCGGTTGGAAAGAGTACGAAATGGAAGTAGTTCGCGACAAAGCG GACAACTGTATCATCGTATGTTCAATCGAAAACTTCGACCCAATGGGCATCCACACCGGTGACTCAATCACGGTT GCTCCAGCGCAAACTCTGACTGACAAAGAATACCAGCTAATGCGTAATGCATCGCTAGCGGTTCTGCGTGAAATC GGTGTTGAGACAGGTGGTTCAAACGTACAGTTTGGTATCAACCCGAAAGATGGCCGTATGGTTATCATCGAGATG AACCCACGTGTATCTCGCTCTTCTGCTCTGGCATCAAAAGCAACAGGTTTCCCAATCGCTAAGATTGCGGCGAAA CTGGCTGTTGGCTTTACTCTAGACGAGCTGCAAAACGACATTACAGGTGGTGCAACTCCGGCATCATTCGAACCT ACTATCGACTACGTAGTGACCAAGATTCCTCGTTTTAACTTCGAGAAATTTGCTGGCGCTAACGATCGACTGACG ACTCAGATGAAGTCAGTTGGTGAGGTAATGGCGATTGGTCGTAACCAACAAGAATCTCTTCACAAAGCATTACGT GGCCTAGAGGTTGGCGCGACTGGCTTTGATGAGATGGTTGACCTAGATGCACCTGACGCATTAACTAAGATTCGT CACGAACTAAAAGAAGCTGGCGCAGAGCGTATCTGGTATATCGCAGATGCATTCCGTGCGGGCATGTCAGTGGAT GGCGTGTTTAACCTGACGAACATTGATCGCTGGTTCCTAGTTCAAATTGAAGAGCTAGTTAAACTAGAAGAGCAA $\tt GTGAAAGCCGGTGGCTTTGCTGGTCTAACAGAAGAAGTTCTACGCCAGATGAAACGTAAAGGTTTCTCTGATGCT$ $\tt CGCCTATCTAAACTGTTAGGTGTGGCGGAAAGCGAAATCCGTCGTCTACGTGACCAGTTTGACATCCACCCTGTC$ TACAAGCGAGTGGATACGTGTGCGGCTGAGTTCTCTTCTGATACGGCTTACATGTACTCATCTTACGATGAAGAG TGTGAAGCAAACCCAACAGATAAAGACAAGATCATGGTACTGGGCGGTGGTCCAAACCGTATCGGTCAAGGTATC GAATTCGACTACTGTTGTGTACATGCATCACTAGCGCTTCGTGAAGATGGCTACGAAACCATTATGGTGAACTGT AACCCAGAAACAGTATCGACAGACTACGATACATCTGACCGTCTTTACTTCGAACCAGTAACTCTTGAAGATGTG TTGTCTATCGCCCGCGTTGAAAAGCCAAAAGGTGTGATTGTTCAATACGGTGGTCAAACGCCACTTAAACTGGCT CGCGCACTAGAAGCTGCAGGCGTGCCAATCATCGGTACAAGCCCGGATGCGATTGACCGCGCAGAAGACCGTGAG

75/160

CGTTTCCAGGCTGCAGTTGAGCGTTTAGGTCTTCTACAACCACAAAACGCAACAGTAACGGCGATGGAGCAAGCG GTTGAGAAATCTCGTGAAATCGGCTTCCCACTCGTTGTTCGTCCATCTTACGTTTTGGGTGGTCGTGCGATGGAA CTAGACCGATTCCTAGATGATGCAACAGAAGTGGATATCGACGCTATCTGTGACGGTGAGCGCGTGGTTATCGGC GGCATCATGGGGCACATTGAGCAAGCGGGCGTTCACTCTGGTGACTCTGCATGTTCGCTTCCTGCTTATACACTA AGCCAAGAAATCCAAGACAAGATGCGTGAGCAAGTTGAGAAGCTGGCGTTCGAACTTGGTGTACGTGGCCTGATG AACACGCAGTTTGCTGTAAAAGACAACGAAGTTTACCTAATTGAAGTAAACCCTCGTGCTGCGCGCTACGGTACCA TTCGTATCGAAAGCGACAGGCGCACCACTAGCGAAAATCGCGGCACGTGTAATGGCGGGTCAATCTCTGGAATCA CAAGGTTTCACTAAAGAGATTATTCCTCCTTACTACTCAGTCAAAGAAGTCGTTCTACCTTTCAATAAGTTCCCT GGCGTTGACCCTCTATTAGGTCCTGAAATGCGCTCAACAGGTGAAGTGATGGGTGTTGGTGCTACGTTTGCAGAA GCTTACGCAAAAGCAGAGCTTGGCTGTGGCAGTGTGTACCCTGAAGGTGGTCGTGCGCTACTTTCTGTTCGTGAA GGTGATAAGCAGCGTGTTGTTGACCTTGCGTCTAAGCTAGTAAAATTGGGTTACCAATTGGATGCGACTCACGGT ACTGCTGTAATCCTTGGTGAAGCGGGTATTAACCCTCGCCTGGTAAACAAAGTACATGAAGGTCGTCCACACATT CTTGACCGCATCAAGAACAACGAATACACCTACATTGTGAACACGGCTGCAGGTCGTCAAGCTATTGAAGATTCG AAAGTTCTACGCCGCGGTGCTCTAGCAGAAAAAGTGAACTACACAACAACGCTAAACGCTGCGTTTGCAACGTGT ATGTCTCACACTGCTGATGCAAAAGCGTCAGTAACTTCTGTTCAGGAGCTACACGCTAAAGTAAAAGCGAGTCTG GAAGCGTAA

253. Vibrio fischeri (SEQ ID NO. 253)

ATGCCAAAACGTACTGATATTAAAAGCGTTCTAATTCTAGGTGCCGGTCCAATTGTAATCGGCCAAGCATGTGAA TTTGACTACTCTGGTGCACAAGCATGTAAAGCACTTCGTGAAGAAGGCTACCGTGTTATTCTTGTGAACTCTAAC CCAGCAACAATCATGACTGACCCAGACATGGCTGATGCAACGTACATTGAACCAATTCATTGGGAAGTGGTTCGT AACATCATCGAAAAAGAGCGTCCAGATGCGGTATTACCAACAATGGGTGGTCAAACAGCATTAAACTGTGCGCTT GATTTAGAAAAGCACGGTGTTCTTGCTGAATTCGGTGTTGAGATGATTGGTGCAACAGCTGATGCAATTGATAAG GCGGAAGACCGTTCTCGTTTTGATAAAGCGATGAAGTCTATTGGACTTGAGTGTCCACGTGCTGATACAGCAAAA GGTACGGGCGGTGGTATCGCATACAACAAGAAGAGTTCGAAGAAATTTGTCGTCGCGGTTTAGACCTTTCGCCA ACTAACGAGCTTCTAATCGATGAATCATTAATCGGTTGGAAAGAGTACGAGATGGAAGTGGTTCGTGATAAGAAC GATAACTGTATCATCGTATGTGCAATTGAAAACTTTGATGCGATGGGTATTCACACTGGTGACTCAATCACGGTT GCGCCAGCACAAACGCTAACGGATAAAGAATACCAACTAATGCGTAATGCATCTCTAGCTGTACTGCGTGAGATT GGTGTTGAAACGGGTGGCTCAAACGTACAGTTTGGTATTAACCCGAAAGATGGTCGTATGGTTATCATCGAAATG AACCCACGAGTATCTCGTTCATCTGCACTTGCTTCTAAAGCAACAGGTTTCCCTATTGCAAAAATTGCAGCGAAA TTGGCTATTGGCTTTACGCTTGACGAGCTAATGAATGACTTACAGGTGGGGCAACGCCTGCGTCATTTGAACCA ACAATCGATTACGTTGTTACTAAGATCCCTCGTTTTAACTTCGAAAAATTCGCAGGGGCTAACGATCGCCTAACA ACACAGATGAAATCAGTTGGTGAAGTGATGGCTATCGGCCGTAACCAACAAGAATCTCTACAAAAAGCACTTCGT GGCCTAGAAGTAGGTGCGACTGGTTTTGATGAGATGGTTGATTTAGATGCTCCTGATGCATTAACAAAAATTCGT CATGAACTGAAAGATGCTGGTGCTGAGCGTATTTGGTACATCGCTGATGCGTTCCGTGCGGGTATGTCTGTTGAT GGTGTGTTTAATCTAACGAATGTTGATCGTTGGTTCCTAGTTCAAATTGAAGATTTAGTAAAAGAAGAAGAAGCG GTTAAAGCGGGTGGTTTTGCTAATTTAACCGCAGATGCACTTCGTAAACTTAAGCGTAAAGGTTTTGCTGATGCG CGTCTTTCTAAACTATTGGGCGTTGGTGAGAGTGAAATTCGTCGCCTGCGTGACCAGCATGATATTCACCCTGTA

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TACAAGCGTGTAGATACGTGTGCTGCTGAGTTCTCATCAGATACGGCTTACATGTACTCATCTTATGATGAAGAG TGTGAAGCAAATCCAACAGACAAAGATAAGATCATGATCTTAGGTGGCGGTCCAAACCGTATCGGTCAAGGTATT GAGTTTGATTACTGTTGTGTACACGCATCATTAGCACTACGAGAAGATGGCTACGAAACTATCATGGTTAACTGT AACCCTGAGACTGTTTCTACGGATTACGATACGTCTGACCGTCTATACTTCGAACCAGTTACTCTAGAAGATGTA $\verb|CTAGCAATTGCTCGTGTTGAGAAACCAAAAGGCGTGATAGTTCAGTACGGTGGTCAAACTCCACTTAAACTGGCT|\\$ $\verb|CGCGCTCTTGAAGCAGCTGGTGTTCCAATCATAGGTACAAGCCCTGATGCTATCGACCGTGCAGAAGACCGTGAG|\\$ CGTTTCCAAGTTGCTGTCGACCGTTTGGAGCTTCTTCAACCAGAAAATGCAACGGTTACTACAATGGAGCAGGCG ATTGATAAATCAAAAGAAATCGGCTTCCCACTCGTAGTACGTCCTTCTTATGTTCTTGGTGGTCGTGCGATGGAA ATCGTATATGACGAGCAAGACTTACGTCGTTACTTCAATGAAGCAGTAAGCGTATCAAATGAATCTCCAGTACTT $\tt CTTGATAGCTTCCTTGATGATGCTGTAGAAGTGGATGTTGATGCGATTTGTGACGGTGAGCAAGTGGTTATCGGC$ GGTATCATGGAGCACATCGAGCAGCGGGTGTTCACTCTGGTGACTCAGCATGTTCTCTTCCTGCTTATACATTA AGCGAAGAATCCAAGATGTAATGCGTGATCAAGTACGTAAGCTGGCATTCGAGCTAGGTGTTCGTGGCTTAATG AATACACAGTTTGCTGTTAAAGATAACAAAGTATACCTAATCGAAGTTAACCCACGTGCTGCTCGTACGGTTCCA $\verb|TTCGTATCGAAAGCAACTGGTGCACCATTAGCTAAGATTGCAGCGCGTGTAATGGCGGGTCAATCTCTAGAGTCT|$ CAAGGCTTTACTAAAGAGATCATCCCACCATACTACTCAGTTAAAGAAGTGGTATTACCGTTCAACAAATTCCCT GGTGTTGACCCACTGTTAGGCCCAGAAATGCGCTCAACGGGTGAAGTTATGGGTGTTGGTACAACGTTTGCTGAA GCATTTGCTAAAGCTGAACTTGGCTGTAGCAAAGAATACCCAGAAGGTGGTCGTGCATTACTTTCTGTTCGTGAA GGTGATAAGAACGTGTTGTAGATTTAGCAAAACATCTTGTTAAATTGGGTTACCAACTGGATGCAACTCACGGT ${\tt ACAGCAGTTATTCTTGGCGAAGCGGGTATTAACCCACGTCTAGTAAACAAGGTACATGAAGGCCGTCCTCATATT}$ $\verb|CTTGACCGTATCAAGAATGGTGAGTACACCTACATCGTTAATACTGCAGCAGGTCGTCAAGCGATTGAAGATTCT| \\$ AAAGTATTACGTCGTGGTGCACTAGCTGAGAAAGTAAACTACACAACACGCTAAATGCAGCATTTGCTAGTTGT TTAGCTCATGAAGCGGATGACCGTAAAACGGTTAACTCTGTTCAAGAGCTACACGCTAAAGTGGCAGCTAAATAC GCTTAA

254. Campylobacter jejuni (SEQ ID NO. 254)

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TCTTTAAGTGGTTTTGATAGGGTAAAATTTGAAGATAGAAATGATCTTGTTTTTAAAATTCGCAATGCCAATGAA AAGCGTTTACTTTATGTTGCTCAAGCTTTTAGGGAAGGTTTTAGCGTAGAAACTTTATGAGCTTTGTAAAATA GATCCTTGGTTTTTAACACAGATTAAAGAAATTGTAGATTTTGAAGAACAATTGATATGGATATTTTAAACAAT AATTTAGAATTAAGCCAAAATGATATTTATTATGTAAGAATGAAGCAAAAAATCATCGCAGAATTTAGTGAAGTG GGTATAGAATTTGACTATGCTTGCGTACATGCTTCTTTTGCGCTTAAAGATATGGGTATTAAAACTATTATGTAT AATTGTAATCCTGAAACCGTTTCGACTGACTATGATACAAGTGATATTTTGTATTTCGAGCCTATTGATTTCGAA ${\tt CATTTAAGAGCGGTGATTGAGCGTGAAAAACCTGATGGAGTGATTGTGCATTTTGGTGGACAAACTCCTTTGAAA}$ TTTGCTAAGCGTTTAAGTGCTTTTGGAGCTAAGATTATAGGTACTAGCGCAAGAGTAATTGATATGGCAGAAGAT GAAGCGGTTCTTAAGGCTAGTGATATAGGGTATCCTGTGCTTGTAAGACCAAGTTATGTTTTAGGTGGGCGTGCG ATGCGCGTGGTAAATGATGAGGCTGAACTTAGACTCTATATGCAAGAAGCTGTGGATGTAAGCCGATAAAAGCCCT GTTTTGATCGATCAGTTTTTAGACAATGCTACAGAAATTGATGTTGATGCGATTTGTGATGGCAAAGATGTTTAT AATATCGATGAAAAAATGCAAGAATTTATTGCACAAAAAACCGCAGATATTGCTTTAAATTTGGGAGTTGTAGGA $\tt CTTTTAAATATACAATTTGCTTTACATAATAATGAGCTTTATATGATGAGGGTAAATCCTAGAGCTAGTCGTACC$ ATACCTTTTGTTAGTAAAGCTACGGGTATTCCTTTAGCAAAAGTGGCAACGCGTGTGATGTGGCAAGGAAATTTA AAAGAAGCTTTAAAATTTTATGATACTTTTAAAGTGGTTAATTTTGATACTAAAATTTTACGCCCTAAAACTCCA AAATATATGAGCGTGAAAGCAGTATTTCCATTTGCAAAACTTAGTGGAAGTGATTTAGAATTAGGTCCTGAA ATGCGTTCAACGGGTGAAGTTATGGGTATAAGCAAGGATTTTGCAAATTCTTATGCGAAAAGTCAAATTGCATCG TTTAATCATCTTCCAGAGCAAGGCGTGGTATTTATCTCCTTAAAAGATAAGGATAAAAAATATACCAAAAAAATC GCTGCAGAATATGTAAAGCTTGGCTTTAAGCTTATGGCAACAGGGGGAACTTGCAAGGAAATTTTAGAAAGTGGT TTTGAGTGCGAACTTGTACATAAAATTTCAGAAGGACGCCCCAATGTTGAAGATAAATTGAAAAATGGAGAAATT CACTTAGTTATCAATACAAGCGATAGTCACAGTTTTAAAGGCGATACGAAAAAAATTCGTGAAAATATTATTCGT TTTAAAATACCTTATTTTACAAATTTACGATCAGCTTTAGCAGGTGCAAAATCGATTAAAGCTATACAGAGTAAA TCTTGCCTAGATGTAAAGAGTTTGCAAGAGTGGCTTAAATCTTGA

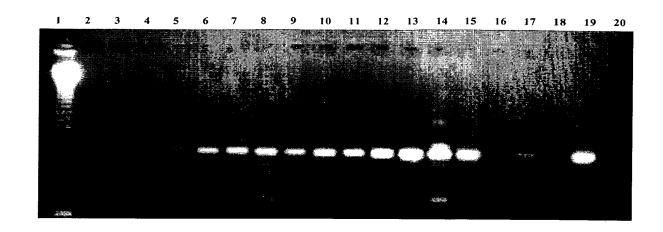
255. Corynebacterium diphtheriae (SEQ ID NO. 255)

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ATGCGTGATGGTGATAACGTTGTGGTTATTTGTTCCATTGAAAATGTTGATGCACTAGGCGTACACAGGT GATTCTGTTACTGTCGCACCTGCTTTGACTCTGACTGATCGTGAATACCAAAAGATGCGTAATCAAGGCATCGCG ATTATTCGTGAAGTAGGGGTCGACACCGGTGGATGTAACATCCAATTTGCGGTAAATCCACGTGATGGTCGTTTG ATCACCATTGAGATGAATCCTCGTGTATCTAGGTCATCCGCCCTTGCATCGAAAGCAACGGGATTCCCCATCGCT AAGATTGCTGCCAAGTTGGCTATCGGATACACGCTGGATGAAATTACTAATGACATCACCGGTGTTACGCCGGCG GCTTTCGAGCCAACGCTCGATTACGTAGTAGTCAAGTCTCCGCGCTTTGCGTTTGAGAAGTTCACAGGATCCGAC GACACATTGACTACAACGATGAAGTCCGTTGGTGAGGCAATGGCTCTTGGCCGTAATTACATCGCGGCGTTGGGT AAAGTCATGCGTTCGCTAGAAAACAAGCAAGTTGGTTTCTGGACAACAAGTGATGAATTCTTTGCTGGGGATCGC GCTAAGAATCTTGACGCAGTGTTAGAAGATCTGAAACGCCCGACAGAAGGGCGGATGTATGACGTGGAGCTGGCT $\tt CTTCGCCTTGGCGGCTCAATTGAAGAAGTACATCAAGCGTCTGGGCTTGATCCATGGTTCTTGGCGGAGCTTCAGCTTCAGGTTCTTGGCGGAGCTTCAGGTTCTTGAGGTTCTTGGCGGAGCTTCAGGTTCTTGAGGTTCTTGAGGTTCTTGAGGTTCTTGAGGTTCTTGAGGTTCTTGAGGTTCTTGGCGGAGCTTCAGGTTCTTGAGGTTTGAGGTTTGAGGTTGAGGTTTGAGGTTTGAGGTTTGAGGTTGAGGTTTGAGGTTGAGGTTGAGGTTGAGGTTTGAGGTTGAGGTTGAGGTTCTTGAGGTTGAGGTTTGAGGTTGAGGTTCTTGAGGTTTGAGGTTGAGGTTGAGGTTCTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTG$ TCATTAATAGATTTCCGAGAATCCTTGATGAAGGCACCGGTGCTGGATGAGCCGTTGCTTCGAAAAGCCAAATTC TTCGGATTGTCTGACCGCCAAATCGCGGCCCTTCGTCCCGAATTTGCAGGGGAAGACGGCGTTCGTCGCTTGCGA TGGTCATTGGGAGTACGCCAGTATTTAAGACTGTAGATACGTGCGCTGCAGAATTTGAAGCTACGACTCCATAC CATTATTCAGCATATGAACTCGATCCAGCTGCTGAATCGGAAGTACGTCCTCAAACTGAAAAAGACAAGATCATC ATTTTGGGATCAGGTCCGAACCGAATTGGCCAAGGTATTGAGTTTGACTACTCATGTGTTCATGCTGCGCTCGAA CTTTCACGCGTGGGGTATGAGACAGTTATGGTTAACTGCAACCCAGAAACCGTGTCGACAGATTATGACACCGCT GACCGTCTGTATTTCGAGCCACTGACATTTGAAGATGTTATGGAGGTCTACCACGCCGAATCAGAATCTGGACAT GTTGCCGGTGTGATCGTTCAGCTTGGCGGACAAACTCCACTTGGACTAGCCGAAAAGCTTCGTGATGCGGGTGTC $\tt CCGGTCATTGGTACTACTCCAGAGGCTATCGATCTAGCTGAAGATCGAGGAGAATTCGGTGAAGTATTGCGTAAA$ GCGCAATTGCCAGCTCCAGCTTTCGGTACCGCTACATCATTTGAGGAAGCTAAAACTGTTGCCAATAACATTGGT TACCCAGTATTAGTTCGTCCATCTTACGTCTTGGGCGGCCGTGGCATGGAAATCGTATACGACGAAAATTCCTTG CACGCGTACATCGAGCGAGCTACCGAGATCACGAGTGATCACCCAGTGCTCGTGGATCGCTTTTTAGATAATGCG ATTGAAATTGACGTTGATGCGCTTTGTGATGGCGAAAATGTCTACCTTGCTGGTGTTATGGAACACATTGAAGAA GCTGGTATTCACTCCGGTGACTCTGCTTGTGCGCTGCCACCTATGACGCTAGGTGCCGAAGATATCGAAAATGTC CGTCGCTCAACAGAAGCGTTGGCACATGGTATCGGCGTTAAAGGATTGATGATGATGTTCAATATGCCTTGAAGGAT GACATTCTTTATGTGATTGAGGCCAACCCTCGTGCATCTCGTACAGTGCCTTTTGTCTCCAAAGCTACGGGTGTC CACTTAGCAAAAGCAGCAGCGCGAATCATGACTGGGGCAACGATTCCTGAGCTTCAAGCGGAGGGAATGATTCCA TTCCGTCGTCCTGATGGCACAATGTTGGATACTTTGCTAAGTCCTGAGATGAAATCAACGGGCGAAGTCATGGGG CTGGCTGATAATTTTGGTGCTGCATATGCTAAGGCAGAACAGGCGGCTTTTGGTGCACTTCCAACTGAAGGCACT GTCTTCGTATCAGTAGCAAACCGCGATAAGCGTACTTTGATTTTCCCAATTCAGCGCCTAGCTTCACTTGGATTC CGAGTACTGGCAACATCAGGCACAGCCGGAATGCTACGTCGCAATGGTATTGAATGCGAAGTTGTATTGAAGCAG ACCCAAGTGCAGGAAGCACGACAAAACGGCACTGAGGGGCAGCGTTCCGTAGTGGATATGATTAAAGCCGGCGAG GTGGACCTCATTCTTAATACACCTGCAGGGTCTTCAGGAGCGCGTCACGACGGTTACCAGATTCGCGCAGCGGCA GTCAACGTTGGCGTTCCTCTGGTTACTACCGTGCAAGGTGTTACTGCGGCAGTACAGGGAATCGAAGCGCTTAGG GCTGGTGAGCTCAGCGTTCGAGCGCTGCAAGAGCTAGATCATTCGGTGACTCGATGA

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Figure 10. Amplification of molecular marker VI (pgi) in Gram-negative bacteria



- 1. DNA Ladder (123 bp)
- 2. Pseudomonas aeruginosa
- 3. Pseudomonas diminuta
- 4. Stenotraophomas maltophilia
- 5. Pseudomonas pseudoalcaligenes
- 6. Burkholderia cepacia
- 7. Pseudomonas putida
- 8. Pseudomonas syringae
- 9. Providencia stuartii
- 10. Proteus mirabilis
- 11. Proteus vulgaris
- 12. Citrobacter freundii
- 13. Enterobacter aerogenes
- 14. Klebsiella oxytoca
- 15. Klebsiella pneumoniae
- 16. Haemophilus influenzae
- 17. Leigonella pneumophila
- 18. Serratia liquefasciens
- 19. Serratia marcescens
- 20. Negative control

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Figure 11. Molecular marker VI (pgi) sequences amplified from different Gram negative bacteria (SEQ ID NOs 256-277).

- TATGGTNNGCGATTGGCCTATCCATTATCTTGTACCGTGGGTTATGACAATTTTGTTCAGCTCCTCGAAGGGGCT
 CATGCAATGGATAAGCACTTTACCCAAACGGCTTTTGAAAAGAATATTCCTGTTCTCCTTGGCTTAATTGGCATT
 TGGTATAACAACTTTTTTGAGTCGGAAACTGAAGCGATTCTGCCATATGATCAATATATGCACCGTTTTGCCGCT
 TATTTCCAACAAGGAAATATGGAGTCAAATGGTAAGTATATTGACCGTAATGGCAACAAAGTTTCTTATCAAACG
 GGGCCAATTATTTGGGGTGAACCGGGCACGAACGGCCAACATGCCTTTTATCAATTGATCCATCAAGGAACTAAA
 ATGATCCCTTGTGATTTTATTGCGCCAGCAGTAACGCATAATCCACTCGGTGATCATCACGATAAATTACTGTCG
 AACTTCTTCGCC
- 257. Enterobacter cloaceae (SEQ ID NO. 257) ECLO
 CTTTGTGGTNCTGCGATCGGCCTGTCTATCATTCTCTCCGTGGGCTTCGACAACTTTGTTGAGCTGCTCTCCGGC
 GCGCACGCGATGGACAACACTTCTCCACCACCGCACCTGAGAAAAACCTGCCGGTGCTGCTGGCGCTGATCGGT
 ATCTGGTACAACAACATTCTTCGGCGCAGAGACCGAAGCGATCCTGCCGTACGACCAGTACATGCACCGCTTCGCG
 GCTTACTTCCAGCAGGGCAATATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCGGTGGATTACCAG
 ACTGGCCCAATCATCTGGGGTGAGCCAGGCACCAACGGTCAGCACGCGTTCTACCAGCTGATTCACCAGGGGACC
 AAAATGGTACCGTGCGATTTCATCGCCCCGGCTATCACCCACAATCCACTGTCTGATCACCATCCTAAACTGCTG
 TCTAACTTCTTCGCCC

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260. Enterobacter aerogenes (SEQ ID NO. 260) EAER

CTGTGGTCCGCCTCGGTCTGTCTATCATTCTGTCCGTCGGCTTCGACAACTTCGTTCAGCTGCTGTCCGGCGCCC

ACGCCATGGACAACACTTCTCTACCACGCCGGCTGAGAAAAACCTGCCGGTACTGCTGGCGCTGATTGGTATCT

GGTACAACAATTTCTTCGGCGCCGAAACCGAAGCAATTCTGCCGTACGATCAGTACATGCATCGCTTTGCCGCTT

ACTTCCAGCAGGGCAACATGGAATCCAACGGTAAGTACGTTGACCGTAACGGCAACGTCGTGGATTACCAGACTG

GCCCTATCATCTGGGGCGAGCCGGGGACTAACGGTCAGCACGCGTTCTATCAGCTGATCCACCAGGGCACCAAAA

TGGTACCGTGCGATTTCATCGCCCCGGCTATCACCCATAACCCGCTGTCTGACCACCATCAGAAACTGCTGTCTA

ACTTCTTCGCAA

- 261. Klebsiella pneumoniae (SEQ ID NO. 261) KPNE

 CTGTGGTCGGCGATTGGTCTGTCCATCATTCTCTCCGTGGGCTTCGACAACTTCGTTGAGCTGCTGTCCGGCGCG

 CATGCGATGGATAAGCACTTCTCCACCACTCCGGCGGAGAAAAACCTGCCGGTGCTGCTGGCGCTGATCGGCATC

 TGGTACAACAACATTCTTCGGTGCGGAAACCGAAGCGATTCTGCCGTACGACCAGTACATGCACCGCTTTGCCGCT

 TACTTCCAGCAGGGCAACATGGAGTCCAACGGTAAGTATGTTGACCGTAACGGCCACGCGGTAGACTACCAGACT

 GGCCCAATCATCTGGGGTGAGCCGGGCACCAACGGTCAGCACCGCTTCTACCAGCTGATCCACCAGGGCACCAAA

 ATGGTACCGTGCGATTTCATCGCTCCGGCTATCACCCACAACCCGCTGTCTGACCACCATCAGAAACTGCTGTCT

 AACTTCTTCGCNAA

- 264. Citrobacter freundii (SEQ ID NO. 264) CFRE
 NTGTGGTCTGCAATCGGCCTGTCCATCATCCTGTCCGTAGGCTTCGACAATTTTGTTGAGCTGCTCTCCGGCGCG
 CATGCGATGGACAAACACTTCTCCACCACCCCCGGCTGAGAAAAACCTGCCGGTGCTGCTGCGCGTGATCGGTATC

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TGGTACAACAACTTCTTCGGTGCCGAAACCGAAGCGATTCTGCCGTATGACCAGTATATGCACCGTTTCGCGGCC
TACTTCCAGCAGGGCAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAATGCGGTGGATTACCAGACT
GGCCCAATCATCTGGGGTGAGCCGGGTACTAACGGCCAGCATGCGTTCTACCAGCTGATCCACCAGGGCACCAAA
ATGGTGCCGTGCGATTTCATCGCGCCGGCAATCACCCACAACCCGCTGTCGGATCACCATCCGAAACTGCTGTCT
AACTTCTTCGCAA

- 266. Serratia marcescens (SEQ ID NO. 266) SMAR

 TGTGGTCGGCGATCGGTTTGTCGATTGCGCTGTCCATCGGTTATGACAACTTCGAGCAGCTGCTGAGCGGCGCGC

 ACGCCATGGACAAGCACTTCGCCGAAACGCCGGCGGAGAAAAACCTGCCGGTGTTGCTGGCGCTGATCGGTATTT

 GGTACAACAACTTCTTTGGCGCCGAAACCGAAGCCATTCTGCCGTACGATCAGTACATGCACCGTTTTGCCGCTT

 ACTTCCAGCAGGGCAACATGGAATCCAACGGCAAGTACGTCGATCGCAACGGCAACCCGGTGGATTACCAGACCG

 GTCCCATCATTTGGGGCGAGCCGGGCACCAACGGCCAGCATGCGTTCTATCAGTTGATCCACCAGGGCACCAAGC

 TGGTGCCGTGCGATTTCATCGCGCCGGCCATCAGCCATAACCNGCTGGGCGATCATCACGCCAAACTGCTGTCCA

 ACTTCTTGCCAA
- GTGGTCGGCGATTGGTCTATCGTGCTCTCTGTCGGTTATGACAACTTCACGCAGTTGCTCGATGGTGCGTA
 TGCCATGGACAAGCACTTCACCGAAACTGAATTCTCACAGAATATTCCGGTGCTGCTGGTGCTGTG
 GTACAACAATTTCTTCGGTGCGGAAACAGAAGCAATTCTGCCTTATGATCAGTACATGCACCGCTTTTGCGGCCTA
 TTTCCAGCAGGGCAATATGGAGTCCAACGGGAAATATTGTGGATCGTAACGGTAAGGTGGTTTCTCATCAGACCGG
 TCCGGTTATCTGGGGTGAGCCCGGCACCAACGGGCAGCATGCGTTTTATCAGCTGATCCATCAGGGTACCAAACT
 GATCCCGTGTGATTTTATCGCACCGGCTCAGAGCCATAATCCGCTGGGGGATCATCACAGTAAACTGCTGTCGAA
 CTTCTTCGCCAA
- 268. Klebsiella oxytoca (SEQ ID NO. 268) KOXY

 GTGGTAGCCTCGGCCTGTCCATCATCCTGTCCGTGGGCTTCGACAACTTTGTTGAGCTGCTCTCCGGCGCGCACG

 CGATGGATAAACACTTCTCCACCACCCCGGCTGAGAAAACCTGCCGGTGCTGCTGGCGCTGATCTGGT

 ACAACAACTTCTTCGGCGCTGAAACCGAAGCGATTCTGCCGTACGACCAGTATATGCACCGTTTTGCCGCTTACT

 TCCAGCAGGGCAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGACGGGCC

 CAATCATCTGGGGCGAGCCGGGGACCAACGGTCAGCACGCGTTCTACCAGCTGATTCACCAGGGGACCAAAATGG

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TGCCTTGCGACTTTATCGCGCCGGCGATTACGCATAACCCGCTGTCCGATCACCATCCGAAGCTGCTGTCTAACT
TCTTCGCCCAA

- 269. Shigella sonnei (SEQ ID NO. 269) SSON
- 270. Salmonella enteritidis (SEQ ID NO. 270) SENT

 GCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTCGAGCTGCTTTCCGGCGCG
 CACGCGATGGACAAGCATTTCTCCACCACTCCGGCGGAGAAAAAACCTACCCATTCTGCTGGCGTTGATTGGCATC
 TGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCGCC
 TACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAGCGGCAACGCCGTGGATTACCAGACA
 GGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTCACCAGGGTACTAAA
 ATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCAGAAGCTGCTGTCT
 AACTTCTTCGCAA
- 271. Salmonella enterica hadar (SEQ ID NO. 271) SHAD

 CGCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTCGAGCTGCTTTCCGGCGC
 GCACGCGATGGACAAGCATTTCTCCACCACTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCAT
 CTGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCGC
 CTACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAGCGGCAACGCCGTGGATTACCAGAC
 AGGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTCACCAGGGTACTAA
 AATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTC
 TAACTTCTTCGCAA
 - 272. Salmonella enterica brandenburg (SEQ ID NO. 272) SBRA

NCGCTGTGGTCTGCCTCGGGCTATCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTCGAGCTGCTTTCCGGCG
CACACGCGATGGACAAGCATTTCTCCACCACTCCGGCGGAGAAAAACCTACCCGTTCTGCTGGCGTTGATTGGCA
TCTGGTACAACAATTTCTTCGGCGGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCG
CCTACTTCCAGCAGGGCAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGA
CAGGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTCACCAGGGTACTA
AAATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGT
CTAACTTCTTCGCNAA

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273. Salmonella enterica derby (SEQ ID NO. 273) SDER

GCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTCGAGCTGCTTTCCGGCGCG
CACGCGATGGACAAGCATTTCTCCACCACTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCATC
TGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCGCC
TACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGACA
GGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTCACCAGGGTACTAAA
ATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTCT
AACTTCTTCGCNAA

274. Salmonella enterica virschow (SEQ ID NO. 274) SVIR CGCTGTGGTCTGCCTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTCGAGCTGCTTTCCGGCGC GCACGCGATGGACAAGCATTTCTCCACCACTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCAT CTGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCGC CTACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGAC AGGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTCACCAGGGTACTAA AATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTC TAACTTCTTCCAA

- 275. Salmonella enterica typhimurium (SEQ ID NO. 275) STPMM

 GCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTCGAGCTGCTTTCCGGCGCG
 CACGCGATGGACAAGCATTTCTCCACCACTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCATC
 TGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTATGACCAGTATATGCACCGTTTCGCCGCC
 TACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGACA
 GGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTCACCAGGGTACTAAA
 ATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCAGAAGCTGCTGTCT
 AACTTCTTCGCNAA
- 276. Salmonella enterica paratyphi B (SEQ ID NO. 276) SPTB

 CGCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTCGAGCTGCTTTCCGGCGC
 GCACGCGATGGACAAGCATTTCTCCACCACTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCAT

 CTGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTATGACCAGTATATGCACCGTTTCGCCGC
 CTACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGAC
 AGGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTCACCAGGGTACTAA
 AATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTC
 TAACTTCTTCCAAA
- 277. Serratia liquefasciens (SEQ ID NO. 277) SLIQ
 NTGTGGTCGGCGATTGGCCTGTCTATCGCCCTGTCAGTGGGTTACGAGAATTTTGAACAGTTGCTGAGCGGCGC
 CACGCGATGGACAACACTTCGCGCAAACGCCGGCAGAGCAAAACCTGCCGGTGCTGCTGGCGTTGATCGGTATC
 TGGTACAACAACTTCTTCGGTGCAGAAACCGAAGCTATCCTGCCGTACGACCAGTACATGCACCGTTTTGCCGCT

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TACTTCCAGCAGGCAACATGGAATCCAACGGTAAATATGTCGATCGCAACGGCAATCCGGTGGACTACCAGACC
GGCCCAATCATCTGGGGCCGGCCACCAACGGGCAGCACGCGTTTTACCAACTGATCCACCAGGGGACCAAA
CTGGTGCCTTGTGACTTTATCGCGCCGGCCATCAGCCATAATCCGCTGAGCGACCACCATGCAAAACTGCTGTCG
AACTTCTTCGCCAA

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Figure 12. Molecular marker VII (EG10839 & EG11396 or sfrB & yigC) in Gram-negative bacteria (SEQ ID NOs 278-303).

278. Neisseria meningitidis serogroup A strain Z2491 (SEQ ID NO. 278)

ACAGAAAATCCTCGAAGACACCCTGCTGGAACAATGGCAGTGGCTCAAACCTAAAGAACCGTAAACATCCTGCGT ACACAAATGCCGTCTGAAACGCCCCCACGCTTCAGACGGCAGACCGTAAAACCTACAACCCCAATTCCTCCCAAA ACTTGTTGGTCGCATCCAAACCCATTTTGCCGCCAAGTCCGCTGACGGGGCTGGCGAAGTCGAGGTAGTCGATGG GCGTGTTTTCCATCAAAACGGTATCGCGCACGGGGTCCATGCGCGTGGTTACCGCCCAGATGACTTCTTTCCAGT CGCGCACATCCACCTCATCCACCACAATGATGAATTTGGTGTACATAAACTGGCGCAGGAACGACCAGCAGC CCATCATCACGCGCTTGGCGTGTCCGGCGTACTGTTTTTTCATGCTCACCACCGCCATGCGGTAGGAGCAGCCTT CGGGCGGCAGGTAAAAATCGGTGATTTCGGGGAACTGCTTTTGCAAAAGCGGTACGAACACTTCGTTCAACGCCA TGCGTTCGACCGTAAACACGGGGAAATGGTCCTGCTCGTTGTAATAGCCCGTGTGGTCGCCGTATGGACCTTCCA TACATTTCACCAGTTCCGTCCGCGAACCGCCAGCAGTCCGGCAAACTGGTATTCGCTCAAGGTATCGGGAACGG GCGTTACCGCGCCCAAAATGGTGGCAGGGTCGCAGCCGAGCACGGCGACGGGATACGGCGTATCGGGATTGA TTAATTGTTGGCGGTAAATGCCGAGATTTTTGGCGTTTTTTTGTGCGCCCCGCGCGTGACGGTCAAGCCCCACGTTA CCAGCGGCGCAACGTCTTCCGGCCAGCAATGCTGAATCGGAAGTTGATACAAATCAACGTCTTCGCCTTCCCATA CGATTTCCTGACACGCGCATTTTTCACCACGTTCGGCGCCATGCTCCAAATGTCTTTCAAGAGCGGCAGTTTGG AAAACGCGTCTTTAATGCCTTTGGGCGGTTCGGGTTCTTTCAAATACGCCAGCGTCTGCCCGATTTCGCGCAGCT TGGACACGCTGTCCGCGCCCATGCCCATCGCCACACGTTCGGGCGTGCCGAACAGGTTTGCCAACACGGGATAAT CATAGCGCGTACCGTCGGGCTTAACTGGGTGTTCAAACAACAACGCCGGCCCTTCGGCGCGCACCACGCGGTCGG CGATTTCGGTCATTTCCAAATGCGGGGAAACGGGGTGCGCGATGCGTTTGAGTTTGCCCTGCTGCTCGAGCATGG CGATGAAGTCGCGCAGGTCTTTGTATTTCATATTCATCCTTTTTGTCCTTTTATCCTGAGCAATCCGATTCGGAT ACCGCCCTATCCTTGCCTGCGCTTCGGCATATTCTATGCCGTGATAAAAGTCGCGTACCAGCGGATGTTCGCTG CCTTGATGGAGTTGCAACAAAGGACGTTGACCATCGGGTTGGGTAACGACATTGCAATGCAAACCGAAGGTGTCG GATTCGTAAGGGGGCAGCCGGTTGCAGATCATGCCGAAATAAACGGCGTTTTCAGGGTTG

279. Klebsiella oxytoca (SEQ ID NO. 279)

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280. Salmonella enterica subsp. enterica serovar Paratyphi A (SEQ ID NO. 280)

ATGGACGCCATGAAATATCACGATTTACGCGACTTCCTGACGCTACTTGAGCAACAGGGGGAACTAAAACGCATC ACGCTACCTGTGGATCCTCATCTGGAAATTACGGAAATCGCTGACCGCACGCTGCGTGCCGGTGGACCGCGTTG CTGTTTGAAAGTCCTAAAGGTTACGCCATGCCGGTGCTGTCCAACCTTTTTGGCACGCCAAAACGCGTGGCGATG GGCATGGGGCAGGATGATGTTTCCGCCTTACGGGAAGTGGGTAAATTATTAGCGTTTCTGAAAGAACCTGAGCCG CCGAAAGGCTTTCGCGATCTGTTTGACAAGCTGCCGCAGTTTAAGCAAGTGCTGAATATGCCGACGAAACGGTTA CGCGGCGCCCTTGCCAGCAGAAAATCGCGTCTGGCGATGATGTCGATTTAACGCGTCTTCCTGTCATGACCTGT TGGCCGGACGCCGCCGCCGCTGATTACCTGGGGACTGACGGTAACGCGTGGCCCGCACAAAGAACGGCAAAAC TTGGATTTCAGGAGTGGTTAGCCGCGCGTCCGGGTGAACGTTTCCCGGTCTCCGTCGCATTGGGCGCCGATCCG GCGACGATACTTGGCGCCGTGACTCCTGTTCCCGATACTCTGTCGGAGTATGCCTTTGCGGGCCTGCTGCGCGGC TACATTGAGCCGGGAGAGTGGCCCGGAAGGACCGTATGGCGATCATACGGGCTATTATAATGAAGTGGATAAC TTTCCGGTCTTTACCGTCACGCATATTACGCAGCGTGAGGATGCCATCTATCACTCCACCTATACCGGGCGTCCG CCCGATGAGCCTGCGGTATTAGGGGTGGCGCTCAATGAAGTCTTCGTGCCTATTCTGCAAAAACAGTTTCCGGAA ATCGTCGACTTTTATCTGCCGCCGGAAGGGTGTTCTTACCGCCTGGCGGTAGTGACGATGAAAAAGCAGTACGCT GGTCATGCGAAACGCGTCATGATGGGCGTCTGGTCGTTTTTGCGCCAGTTTATGTATACGAAATTTGTTATCGTT TGCGATGATGACGTTAACGCACGCGACTGGAATGATGTGATCTGGGCGATTACCACCCGTATGGACCCTGCGCGG GATACGGTGCTGGTTGAAAATACGCCGATTGATTACCTGGATTTTGCCTCGCCGGTCTCCGGGCTGGGTTCAAAA ATGGGGCTGGATGCCACAAACAATGGCCGGGCGAAACCCAACGCGAGTGGGGTCGTCCTATTGTTAAAGATCCT GAAGTTACCGCACGTATTGATGCGATTTGGGATGAGCTGGCTATCTTTAAATAA

281. Salmonella typhimurium LT2 (SEQ ID NO. 281)

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282. Escherichia coli CFT073 (SEQ ID NO. 282)

ATGGACGCCATGAAATATAACGATTTACGCGACTTCTTGACGCTGCTTGAACAGCAGGGTGAGCTAAAACGTATC ACGCTCCCGGTGGATCCGCACCTGGAAATCACTGAAATTGCTGACCGCACTTTGCGTGCCGGTGGGCCTGCGCTG TTGTTCGAAAACCCTAAAGGCTACTCAATGCCGGTGCTGTGCAACCTGTTCGGTACGCCAAAGCGCGTGGCGATG CCAAAAGGTTTCCGCGACCTGTTTGATAAACTGCCGCAGTTTAAGCAAGTATTGAACATGCCGACAAAGCGACTG $\tt CGTGGTGCACCCTGCCAACAAAAATCGTCTCTGGCGATGACGTCGATCTCAATCGCATTCCCATTATGACCTGC$ TGGCCGGAAGATGCCGCGCCGCTGATTACCTGGGGGCTCACCGTAACGCGCGGCCCGCATAAAGAGCGGCAGAAT $\tt TTGGATTATCAGGAGTGGTGCGGCGCATCCGGGCGAACGTTTCCCGGTTTCTGTGGCGCTGGGTGCCGATCCT$ GCCACGATTCTCGGTGCAGTCACCCCCGTTCCGGATACGCTTTCAGAGTATGCGTTTGCCGGATTGCTGCGCGGT ACCAAGACCGAAGTGGTGAAGTGTATCTCCAATGACCTTGAAGTGCCCGCCAGTGCGGAGATTGTGCTGGAAGGG ${\tt TATATCGAACAAGGCCGAAACTGCGCCGGAAGGGCCGTATGGCGACCACCGGTTACTATAACGAAGTCGATAGT}$ $\tt TTTCCGGTATTTACCGTGACGCATATTACCCAGCGTGAAGATGCGATTTATCATTCCACCTATACCGGGCGTCCG$ CCAGATGAACCTGCGGTACTGGGTGTAGCACTGAACGAAGTGTTCGTGCCGATTCTGCAAAAACAGTTCCCGGAA ATTGTCGATTTTTATCTGCCGCCGGAAGGCTGTTCTTATCGTCTGGCGGTAGTGACGATCAAAAAACAGTACGCC ${\tt GGACACGCGAAGCGCGTCATGATGGGCGTCTGGTCGTTCTTACGCCAGTTTATGTACACTAAATTTGTGATCGTT}$ TGCGATGATGACGTCAACGCCCGCGACTGGAACGATGTGATTTGGGCGATTACCACCCGTATGGACCCGGCGCG ${\tt GATACTGTTCTGGTAGAAAATACGCCTATTGATTATCTGGATTTTGCCTCGCCTGTCTCCGGGCTGGGTTCAAAA}$ ATGGGGCTGGATGCCACGAATAAATGGCCGGGTGAAACCCAGCGTGAATGGGGGACGTCCCATCAAAAAAGATCCA GATGTTGTCGCGCATATTGACGCCATTTGGGATGAACTGGCTATTTTTAACAACGGTAAAAGCGCCTGA

283. Escherichia coli K12 (SEQ ID NO. 283)

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TATATCGAACAAGGCGAAACTGCGCCGGAAGGGCCGTATGGCGACCACACCGGTTACTATAATGAAGTCGATAGT
TTCCCGGTATTTACCGTGACGCATATTACCCAGCGTGAAGATGCGATTTACCATTCCACCTATACCGGGCGTCCG
CCAGATGAGCCCGCGGGTGCTGGGTGTCGCACTGAACGAAGTGTTTTGTGCCGATTCTGCAAAAAACAGTTCCCGGAA
ATTGTCGATTTTTACCTGCCGCCGGAAGGCTGCTCTTATCGCCTGGCGGTAGTGACAATCAAAAAACAGTACGCC
GGACACGCGAAGCGCGTCATGATGGGCGTCTGGTCGTTCTTACGCCAGTTTATGTACACTAAATTTGTGATCGTT
TGCGATGATGACGTTAACGCACGCGACTGGAACGATGTGATTTGGGCGATTACCACCCGTATGGACCCGGCGCG
GATACTGTTCTGGTAGAAAAATACGCCTATTGATTATCTGGATTTTGCCTCGCCTTGTCTCCGGGCTGGGTTCAAAA
ATGGGGCTGGATGCCACGAATAAATGGCCGGGGGAAACCCAGCGTGAATGGGGACGTCCCATCAAAAAAGATCCA
GATGTTGTCGCGCCATATTGACCCCATCTGGGATGAACTGGCTATTTTTAACAACGGTAAAAAGGATCCA

284. Salmonella enterica subsp. enterica serovar Typhi (SEQ ID NO. 284)

 ${\tt ATGGACGCCATGAAATATCACGATTTACGCGACTTCCTGACGCTACTTGAGCAGCAGGGGGAACTAAAACGCATC}$ ${\tt ACGCTACCTGTGGATCCTCATCTGGAAATCACGGAAATCGCTGACCGCACGCTGCGTGCCGGTGGACCGGCGTTG}$ $\tt CTGTTTGAAAATCCTAAAGGTTACGCCATGCCGGTGCTGTGCAACCTTTTTGGCACGCCAAAACGCGTGGCGATG$ GGCATGGGGCAGGATGATGTTTCCGCCTTACGGGAAGTGGGTAAATTATTAGCGTTTCTGAAAGAACCTGAGCCG CCGAAAGGCTTTCGCGATCTGTTTGACAAGCTGCCGCAGTTTAAGCAAGTGCTGAATATGCCGACGAAACGGTTA CGCGGCGCCCTTGCCAGCAGAAATCGCGTCTGGCGATGATGTCGATTTAACGCGTCTTCCTGTCATGACCTGT $\tt TGGCCGGACGCCGCGCGCTGATTACCTGGGGACTGACGGTAACGCGTGGCCCGCACAAAGAACGGCAAAAC$ $\tt TTGGATTTTCAGGAGTGGTTAGCCGCGCGTCCGGGTGAACGTTTCCCGGTCTCCGTCGCATTGGGCGCCGATCCG$ GCGACGATACTTGGCGCCGTGACTCCTGTTCCCGATACTCTGTCGGAGTATGCCTTTGCGGGCCTGCTGCGCGC TACATTGAGCCGGGAGAGATGGCGCCGGAAGGACCGTATGGCGATCATACGGGCTATTATAATGAAGTGGATAAC $\tt TTTCCGGTCTTTACCGTCACGCATATTACGCAGCGTGAGGATGCCATCTATCACTCCACCTATACCGGGCGTCCG$ $\tt CCCGATGAGCCTGCGGTATTAGGGGTGGCGCTCAATGAAGTCTTCGTGCCTATTCTGCAAAAACAGTTTCCGGAA$ ${\tt ATCGTCGACTTTTATCTGCCGCCGGAAGGGTGTTCTTACCGCCTGGCGGTAGTGACGATGAAAAAGCAGTACGCT}$ GGTCATGCGAAACGCGTCATGATGGGTGTCTGGTCGTTTTTGCGCCAGTTTATGTATACGAAATTTGTTATCGTT TGCGATGATGACGTTAACGCACGCGACTGGAATGATGTGATCTGGGCGATTACCACCCGTATGGACCCTGCGCGG ${\tt GATACGGTGCTGGATACGCCGATTGACTACCTGGATTTTGCCTCGCCGGTCTCCGGGCTGGGTTCAAAA}$ $\tt ATGGGGCTGGATGCCACAAACAAATGGCCGGGCGAAACCCAACGCGAGTGGGGTCGTCCTATTGTTAAAGATCCT$ GAAGTTACCGCGCGTATTGATGCGATTTGGGATGAGCTGGCTATCTTTAAATAA

285. Escherichia coli 0157:H7 EDL933 (SEQ ID NO. 285)

ATGGACGCCATGAAATATAACGATTTACGCGACTTCTTGACGTTGCTTGAACAGCAGGGTGAGCTAAAACGTATC
ACGCTCCCGGTGACCCGCATCTGGAAATCACTGAAATTGCTGACCGCACGCTGCGTGCTGGTGGGCCTGCGCTG
TTGTTTGAAAACCCTAAAGGGTACTCAATGCCGGTGCTGTGCAACTTGTTCGGTACGCCAAAGCGCGTAGCGATG
GGTATGGGCCAGGAAGATGTTTCAGCACTGCGTGAAGTCGGTAAATTATTAGCATTTCTGAAAGAACCAGAGCCG
CCAAAAGGTTTTCGCGATCTGTTTGATAAGCTGCCGCAGTTTAAGCAGGTGTTAAACATGCCGACAAAGCGACTG
CGCGGTGCACCCTGCCAACAAAAAATCGTCTCTGGCGATGACGTCGATCTCAACCGTATTCCCATTATGACCTGT

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286. Shigella flexneri 2a str. 301 (SEQ ID NO. 286)

ATGGACGCCATGAAATATAACGATTTACGCGACTTCCTGACGCTGCTTGAACAGCAGGGTGAGCTAAAACGTATC ACGCTCCCGGTGGATCCGCATCTGGAAATCACTGAAATTGCTGACCGCACTCTGCGTGGTGGGCCTGCGCTG TTGTTCGAAAACCCTAAAGGCTACTCAATGCCGGTGCTGTGCAACCTGTTCGGTACGCCAAAGCGCGTGGCGATG GGCATGGGGCAGGAAGATGTTTCGACGCTGCGTGAAGTTGGTAAATTATTGGCGTTTCTGAAAGAGCCGGAGCCG CCAAAAGGTTTCCGCGACCTGTTTGATAAACTGCCGCAGTTTAAGCAGGTGTTAAACATGCCGACAAAGCGACTG CGTGGTGCCCCTGCCAACAAAAATCGTCTCTGGCGATGACGTCGATCTCAATCGCATTCCCATTATGACCTGC TGGCCGGAAGATGCCGCCGCTGATTACCTGGGGGCTGACCGTAACGCGCGCCCGCATAAAGAGCCGCAGAAT CTGGATTATCAGGAGTGGTGCGGCGCATCCGGGCGAACGTTTCCCGGTTTCTGTGGCGCTGGGTGCCGATCCT GCCACGATTCTCGGTGCAGTCACCCCCGTTCCGGATACGCTTTCAGAGTATGCGTTTGCCGGATTGCTACGCGGC TATATCGATCCTGGTGAGATGGCGCCGGAAGGGCCGTATGGTGACCACACAGGTTACTATAATGAAGTCGATAAT TTCCCGGTGTTTACCGTGACGCATATTACCCAGCGTGAAGATGCGATTTACCATTCCACCTATACCGGGCGTCCG CCAGATGAGCCCGCGGTACTGGGCGTGGCGTTGAACGAAGTGTTTGTACCGATTCTGCAAAAACAGTTCCCGGAA ATTGTCGATTTTTACCTGCCGCAGGAGGCTGTTCTTATCGTCTGGCGGTAGTGACGATCAAAAAACAGTACGCC GGACACGCGAAGCGCGTCATGATGGGCGTCTGGTCGTTCTTACGCCAGTTTATGTACACTAAATTTGTGATCGTT TGCGATGATGACGTCAACGCACCGGACTGGAACGATGTGATTTGGGCCGATTACCACCCGTATGGACCCGGCGCG GATACTGTTCTGGTAGAAAATACGCCTATTGATTATCTGGATTTTGCCTCGCCTGTCTCTGGGCTGGGTTCAAAA ATGGGGCTGGATGCCACGAATAAATGGCCGGGGGAAACCCAGCGTGAATGGGGACGTCCCATCAAAAAAGATCCA GATGTTGTCGCGCATATTGACGCCATCTGGGATGAACTGGCTATTTTTAACAACGGTAAAAGCGCCTGA

287. Pseudomonas aeruginosa PAO1 (SEQ ID NO. 287)

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AAGCCGACCGGCTTCGACATGCCGGTGCTCGGCAACCTGTTCGGTACGCCGGAGCGCGTGGCGCTGGGCATGGGC GCCGAGGACGTCGGCGCACTGCGCGAGATCGGCAAGCTGCTGGCGCAACTCAAGGAGCCCGAGCCGCCGAAGGGC CTCAAGGACGCCTGGGCCAAGCTGCCGATGTACAGGAAGGTCCTGTCCATGGCGCCGAAGGTGCTCAAGGACGCC GATGTCGGGCCGCTGATCACCTGGGGCCTGACCGTTACCCGCGGGCCGAACAAGGAACGGCAGAACCTGGGCATC TACCGCCAGCAGGTGATCGGCCGCAACAAGGTGATCATGCGCTGGCTCAGCCATCGCGGCGCGCACTGGACTAC CGCGAGTGGTGCCAGAAGCATCCGGGCCAGCCCTATCCGGTAGCCGTGGCGCTGGGCGCCGATCCGGCGACCATC CTCGGTGCGGTGACGCCGGACACCCTTTCCGAATACGCTTTCGCCGGCCTGTTGCGCGGGCATCGTACC GAGCTGGTCAAGTGTCGCGGGAGCGACTTGCAGGTGCCGGCCAGCCCGAGATCGTCCTCGAAGGGGTGATCCAC CCCGGCGAGATGGCCGACGAAGGCCCCTATGGCGATCACACCGGCTACTACAACGAGGTCGATCGCTTCCCGGTG TTCACCGTCGAGCGCGTCACCCGCCGGCAGAAACCGATCTACCACAGCACCTACACCGGGCGTCCGCCGGACGAG CCGGCGATCCTCGGGGTGGCCCTGAACGAAGTGTTCGTGCCGATCCTGCAGAAGCAGTTCCCGGAAATCGTCGAT TTCTACCTGCCGCAAGGTTGTTCCTACCGGATGGCGGTGACCATGAAGAAGCAGTACCCAGGGCACGCC AAGCGCGTGATGCTCGGGGTCTGGTCGTTCCTGCGGCAGTTCATGTACACCAAGTTCGTCATCGTCACCGACGAT GACATCGATGCGCGCGACTGGAACGATGTGATCTGGGCCATCACCACGCGGATGGACCCCAAGCGCGACACGGTG ATGATCGACAACACGCCCATCGACTACCTCGACTTCGCCTCGCCGGTTTCCGGCCTCGGCTCGAAGATGGGGGCTT GATGCCACCCACAAGTGGCCGGGCGAGACCAGCCGCGAATGGGGGCGCGCCATCGTCAAGGACGAAGCGGTGACA CGGCGCATCGACGCCTCTGGTCGAGCCTCGGGATCGACTGA

288. Pseudomonas syringae pv. tomato str. DC3000 (SEQ ID NO. 288)

ATGAAATTCAAAGATCTAAGGGATTTCGTGCAGCAGTTGGAGCAGCGCGGAGAGTTGAAACGCATTCAGATGCCG ATCTCGCCTGTGCTGGAAATGACTGAAATCTGTGACCGTACCTTGCGCGCCCAAAGGCCCGGCCCTGCTGTTTGAA AACCCGGTTGGCTTTGATATTCCGGTGCTGGGCAACCTGTTCGGCACGCCGGAGCGCGTGGCCATGGGCATGGGC CTGAAAGATGCCTGGTCCAAGCTGCCCATCTTCCGCAAAGTCATCGCCATGGCGCCCAAGGTCGTCAAGGATGCA CCCTGCCAGGAGATCGTCATCGAGGGTGATGACGTCGATCTCGGCATGTTGCCGGTGCAGACCTGCTGGCCGGGC GATGTCGCGCCGCTGATCACCTGGGGCCTGACCGTGACCAAAGGCCCGAACAAGGAGCGGCAGAACCTCGGTATT TATCGCCAGCAGGTCATCGGCCGCAACAAGATCATCATGCGCTGGCTCAGCCATCGCGGTGGCGCGCTTGACTTC CGCGACTGGTGCGTCAAGCATCCTGGCGAGCCTTATCCGGTGGCCGTCGCACTGGGCGCGGACCCATT $\tt CTCGGTGCCGGTGCCCGACAGCCTGTCCGAATACGCCTTCGCCGGGCTACTGCGTGGCTCGCGCACC$ CCGGGCGAGATGGCCAACGAAGGCCCCTACGGCGATCACACCGGTTATTACAACGAAGTCGACAGCTTTCCGGTG CTCACCGTCGAGCGCATCACCCACCGCATCAAGCCGATCTACCACAGCACCTACACCGGGCGTCCACCGGACGAG CCGGCTATCCTGGGTGTGGCGCTGAACGAAGTGTTCGTGCCGATTCTGCAGAAGCAGTTTCCGGAAATCGTCGAT TTCTACCTGCCGCCCGAGGGGTGCTCTTACCGCATGGCGGTGGTGACTATCAAGAAACAGTACCCCGGCCATGCC AAGCGCGTGATGCTCGGCCGTTCCTGCGCCCAGTTTATGTACACCAAATTTGTGATCGTCACCGATGAC GACATCAATGCGCGTGACTGGAATGACGTGATCTGGGCCATCACCACCGCATGGACCCCAAGCGCGACACGGTC ATGATCGACAACACGCCCATCGATTACCTCGATTTTGCCTCTCCGGTGTCTGGATTGGGATCAAAAATGGGCCTG

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GATGCCACTAACAAATGGCCAGGGGAAACCACCCGCGAATGGGGCAGGGCGATCGTCAAGGACGAAGCCACCACGCGCCGGGTGGACGAGATCTGGACTCAGTTGGGAATAGACTGA

289. Yersinia pseudotuberculosis IP 32953 (SEQ ID NO. 289)

ATGATCAGCATGAAATACCGTGACTTACGTGACTTCCTCTCATTACTGGAACAGAGGGGGGGAACTTAAACGCATT AGCCAGCCCATTGATCCTTATTTGGAAATGACAGAAATTGCCGATCGCACGTTACGTGCTGGTGGGCCTGCGTTA CTTTTTGAGAACCCTAAAGGTTACAGCATGCCCGTGTTGTGTAATCTGTTTGGCACCGCTAAGCGAGTCGCCATG GGGATGGGGCAAGAAGATGTCAGCGCCCTGCGAGATGTTGGTAAATTATTGGCCTTCCTGAAAGAACCCGATCCC CCAAAAGGTTTCCGTGACTTATTTGATAAGCTGCCAAAATTTAAGCAGGTATTGAATATGCCAACGAAACGCTTG AACTCGGCCCCGTGTCAGGAGCAAGTTTGGCAAGGTGAGGATGTTGATTTAAGTCGCATCCCTGTGATGCACTGC TGGCCAGAAGATGCCGCACCACTAGTCTCTTGGGGGTTGACTATTACACGTGGTCCCCACAAAGAACGGCAGAAT $\tt CTGGATTATCAGGAGTGTGAGGCACACCCTGGTGAACGTTTTCCGGTCGCTGTCGCCTTGGGAGCAGACCCT$ GCTACGATCTTAGCCGCAGTGACCCCGGTACCAGACACGCTGTCTGAATATGCCTTTTGCCGGCTTGTTACGCGGC CATAAAACGGAAGTGGTGAAGTGTCTTTCCAATGACCTTGAAGTTCCTGCAAGTGCAGAAATTGTATTGGAAGGA TATATCGAACAAGGTGATATGGCTCCGGAAGGTCCTTATGGTGATCATACGGGCTATTACAATGAAATAGATAAT TTCCCCGTGTTTACCGTCACGCATATTACACAGCGCCAAGACGCAATTTATCATTCAACCTATACGGGCCGACCA $\tt CCGGATGAACCTGCGGTAATGGGGGTGGCACTGAACGAAGTCTTTGTACCTATTTTGCAAAAGCAATTCCCGGAA$ ATTGTTGATTTCTACTTGCCACCAGAAGGGTGCTCATACCGGTTGGCGGTGGTAACCATCAAGAAACAATATGCA GGCCATGCCAAACGCGTGATGATGGGAGTATGGTCGTTTTTACGCCAGTTTATGTATACCAAGTTTGTTATTGTT TGTGATGACGATATTAATGCTCGTGATTGGAATGATGTAATTTGGGCGATCACCACCCGGATGGACCCATCCCGC GATACGGTGTTAATTGAAAATACACCGATAGATTATTTGGATTTCGCCTCACCGGTTTCCGGTTTGGGATCGAAA ATGGGGCTGGATGCCACCAACAATGGCCAGCAGAGACTCCGCGTGAATGGGGGGCGTCCAATTAAGATGGACGAA GACGTCCGTGCCCGTATTGATGCTCTGTGGGATGAGCTGGCCATTTTCAGTGACAAAGACGCGAAACGCTAA

290. Neisseria meningitidis serogroup B strain MC58 SEQ ID NO. 290)

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291. Neisseria gonorrhoeae FA 1090 (SEQ ID NO. 291)

ATGAAATACAAAGACCTGCGCGACTTCATCGCTATGCTCGAGCAGCGGCAAGCTCAAGCGCGTCGCCCACCCC GTTTCCCCGCATTTGGAAATGACCGAAATTGCCGACCGCGTGTTGCGCGCCGAAGGGCCGGCGTTGTTGTTTGAA AACCCGGTTAAGCCCGACGGTACGCCTATGATTATCCCGTGTTGGCGAACCTGTTCGGCACCCCGAACGTGTG GCGATGGGCATGGGCGGACAGCGTGTCCAAGCTGCGCGAAATCGGGCAGACGCTGGCGTATTTGAAAGAACCC GAACCGCCCAAAGGCATCAAAGACGCGTTTTCCAAACTGCCGCTGTTGAAAGATATTTGGAGCATGGCGCCGAAC GTGGTGAAAAACGCGCCGTGTCAGGAAATCGTGTGGGGAAGGAGAAGACGTTGATTTGTATCAGCTTCCGATTCAA CATTGCTGGCCGGAAGACGTTGCGCCGCTGGTAACGTGGGGCTTGACCGTCACGCGCGGGCCGCACAAAAAACGC GGCGCGTTGGATTATCAGGAATTCCGCAAACTCAATCCCGATACGCCGTATCCCGTCGCCGTCGTACTCGGTTGC GACCCCTCCACCATTTTGGGCGCGGTAACGCCCGTTCCCGATACTTTGAGCGAATACCAGTTTGCCGGACTGCTG GAAGGCGTGATTCATCCAAACGAAACCGCGTTGGAAGGCCCATACGGCGACCACACGGGCTATTACAACGAGCAG AAACCGCCCGACGAACCTGCCGTTTTGGGCGTGGCGTTGAACGAAGTGTTCGTACCGCTTTTGCAAAAGCAGTTC TCCGAAATCACCGATTTCTACCTGCCGCCCGAAGGCTGTTCCTACCGCATGGCGGTGGTCAGCATGAAAAAACAG TACGCCGGACACGCCAAGCGCGTGATGACGGGCTGCTGGTCGTTCCTGCGCCAGTTTATGTACACCAAATTCATC ATCGTGGTGGATGACGATGTAAACGTGCGCGACTGGAAAGAAGTCATCTGGGCGGTAACCACGCGCATGGACCCC GTCCGCGACACCGTTTTGGTGGAAAACACGCCCATCGACTACCTCGACTTCGCCAGCCCCGTCAGCGGACTCGGC GACCCTGCGGTTACGGTTAAAATTGATGGGATTTGGGGGAAATTGGGGTTGTAG

292. Yersinia pestis CO92 (SEQ ID NO. 292)

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GCTACGATCTTAGCCGCAGTGACCCCGGTACCAGACACGCTGTCTGAATATGCCTTTGCCGGCTTGTTACGCGGC
CATAAAACGGAAGTGGTGAAGTGTCTTTCCAATGACCTTGAAGTTCCTGCAAGTGCAGAAATTGTATTGGAAGGA
TATATCGAACAAGGTGATATGGCTCCGGAAGGTCCTTATGGTGATCATACGGGCTATTACAATGAAATAGATAAT
TTCCCCGTGTTTACCGTCACGCATATTACACAGCGCCAAGACGCAATTTATCATTCAACCTATACGGGCCGACCA
CCGGATGAACCTGCGGTAATGGGGGTGGCACTGAACGAAGTCTTTGTACCTATTTTGCAAAAAGCAATTCCCGGAA
ATTGTTGATTTCTACTTGCCACCAGAAGGGTGCTCATACCGGTTGGCGGTGGTAACCATCAAGAAACAATATGCA
GGCCATGCCAAACGCGTGATGATGGGGAATATGGTCGTTTTTACGCCAGTTTATGTATACCAAGTTTGTTATTGTT
TGTGATGACGATATTAATGCTCGTGATTGGAATGATGTAATTTGGGCGATCACCACCCGGATGGACCCATCCCGC
GATACGGTGTTAATTGAAAATACACCGATAGATTATTTTGGATTTCGCCTCACCGGTTTCCGGTTTTGGGATCGAAA
ATGGGGCTGGATGCCACCAACAAATGGCCAGCAGAGACTCCGCGTGAATGGGGGCGTCCAATTAAGATGGACGAA
GACGTCCGTGCCCGTATTGATGCTCTGTGGGATGAGCTGGCCATTTTCAGTGACAAAGACGCGAAACGCTAA

293. Pseudomonas putida KT2440 (SEQ ID NO. 293)

TTGATTGGGGCCCTTGCGGGCCCTTCGCGGGCAAGCCCGCTCCTGCACAGGTCATTGCGGCCCTTGTAGGAGCG GGCTTCCGCGAAGGGATGCAAAGCGGCCCCAATGCATTTTCACCCCCAAACAAGGCCCGAACGGCGCTACACTCT GAACAGCGCGGCGAGCTCAAGCGCATCCAGGTACCGATCTCCCCCGTCCTGGAAATGACCGAGGTCTGCGACCGC ACCCTGCGCGCCAAGGGCCCGGCATTGTTGTTCGAAAAGCCCACCGGCTTCGACATCCCAGTGCTGGGCAACCTG TTCGGTACCCCGGAGCGGGTGGCCATGGGCATGGGCGCCGAGTCGGTCAGCGAACTGCGGGAAATCGGCAAGCTG CTGGCCTTCCTCAAGGAGCCTGAGCCGCCCAAGGGCCTGAAGGACGCCTGGTCGAAGCTGCCGATCTTCAAGAAG GTCGTGTCGATGGCGCCAAAAGTGGTCAAGGACGCGGTGTGCCAGGAAGTGGTCGAGGGTGACGATGTCGAC CTTGGCACGCTGCCGATTCAGCACTGCTGGCCTGGCGACGTGGCCCCTGATTACCTGGGGCCTCACCGTGACC CGTGGCCCGAACAAGGACCGCCAGAACCTGGGCATCTACCGCCAGCAGGTGATCGGCCGCAACAAGGTGATCATG CGCTGGCTCAGCCATCGTGGCGGCGCCCTCGATTACCGAGAGTGGTGCGAGAAGAACCCCGGCCAGCCGTTTCCG GTCGCCGTGGCCCTGGCCCTGACCCAGCGACCATTCTCGGCGCGGTGACCCCGGTCCCGGACACCCTTTCCGAG TACGCCTTCGCCGGCCTGCTGCGAGGCAATCGCACCGAGCTGGTCAAGTGCCGTGGCAGCAACCTGCAGGTACCG GCAACCGCCGAGATCATTCTGGAAGGGGTGATCCACCCAGGCGAAATGGCCCCGGAAGGCCCTTACGGCGATCAC TACCACAGCACCTACACCGGCCGGCCGCCAGATGAGCCGGCCATTCTCGGCGTGGCGCTGAACGAAGTGTTCGTG CCGATCCTGCAGAAGCAGTTCCCGGAAATCACCGACTTCTACCTGCCGCCGGAAGGCTGCTCGTACCGCATGGCG GTGGTGACCATGAAGAAACAGTACCCAGGCCACGCCAAGCGCGTAATGCTGGGTGTGTGGTCGTTCCTGCGACAG TTCATGTACACCAAGTTCGTTATTGTCACCGATGACGATATCAACGCTCGTGACTGGAACGATGTGATCTGGGCC ATTACCACGCGCATGGACCCCAAGCGTGATACGGTAATGATTGACAATACCCCGATCGACTACCTGGACTTTGCG TCACCGGTGTCGGGGCTGGGGTTCGAAGATGGGCCTGGACGCTACGCACAAGTGGCCGGGCGAGACTACACGCGAA TGGGGCCGGGTCATCGTCAAGGATGAGGCCGTCACCCGCCGTATCGATGAGCTGTGGGATCAGTTGGGAATAGAT TGA

294. Serratia marcescens ATCC 13880 (SEQ ID NO. 294)

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AGCGCCACGCCCAGGATCGCCGGCTCATCCGGCGGCGGCCGGTGTAGGTCGAGTGGTAGATCGCGTTGCGGCGC
TGGGTGATGTGAGTAACGGTGAACACCGGGAACTGGTCGATTTCATTGTAGTAACCGGTGTGGTCGCCGTAGGGG
CCTTCCGGCGCCATTTCACCCGGCTCGATATAGCCTTCAAGCACGATTTCGGCGCTGGCGGGCACTTCCAGATCG
TTGGAAAGGCACTTGACCACTTCGGTTTTGTTGCCGCGCAGCAACCCGGCAAAGGCGTATTCGGACAAGGTATCA
GGCACCGGCGTGACCGCACCGAGGATGGTAGCAGGATCGGCCCCCGCAACCGGGAAACGCTCGCCC
GGGTGCGCCTGGCACCACTCCTGATAATCCAGCGCCCCGCGCATGCGACAGCCAACGCAT

295. Burkholderia mallei ATCC 23344 (SEQ ID NO. 295)

ATGAAATACAGAGATTTACGCGATTTCATCCATGGCCTCGAGCAGCGCGGCGAGTTGCGGCGCGTCACCCAGCCC GCGCCGGCCGCCACCGGTTTCCGGTGCTCGGCAATCTGTTCGGCACGCCGCGGCGCGTCGCGCTCGGCATGGGC GTCGACGCCGACGACGAGGCGCCTCGCGTCGCTGCGCGACATCGGCCGCCTGCTGTCCGCGCTCAAGGAGCCG ACGGTCTCCGCGCCGCCGTGCCAGGAGATCGTCTGGGGAAGGCGACGACGTCGATCTGCACAAGCTGCCGATCCAG ACCTGCTGGCCGGGCGACGCCGGCCGCTCACGTGGGGCCTGACCGTCACGCGGGCCGAACAAGACGCGC CAGAATCTGGGCATCTACCGGCAGCAACTGATCGGACGCAACAAACTGATCATGCGCTGGCTCGCGCATCGCGGC GGCGCGCTCGATTTCCGCGAATTCGCGCTGAAGCATCCGGGCCAGCCCTATCCCGTCGCCGTCGTGCTCGGCGCC GATCCGGCGACGATGCTCGGGGCCGTCACGCCCGTGCCCGATTCGCTGTCCGAATACCAGTTCGCGGGCCTGCTG GCCGCGGCCGCCGGCTACGAGCATGCGCTCGAGGGCCCGTACGGCGATCACACCGGCTACTACAACGAG ${\tt CAGGAATGGTTTCCGGTCTTCACGGTCGAGCGGATCACGATGCGCCGCGATGCGATCTACCACTCGACGTACACC}$ GGCAAGCCGCCGACGAGCCGGCCGTGCTCGGCGTCGCGCTGAACGAAGTGTTCGTGCCGCTGCTGCAGAAGCAG TTCGCCGAGATCACCGATTTCTATCTGCCGCCCGAGGGTTGCAGCTACCGGATGGCGATCGTCCAGATGAAGAAG AGTTACGCGGGACACGCGAAGCGGGTGATGTTCGGCGTCTGGAGCTTCCTGCGGCAGTTCATGTATACGAAGTTC CCGGCGCGCGACACGGTGCTCGAGAACACGCCGATCGACTATCTCGACTTCGCGTCGCCGGTCGCCGGCCTC ATGGACGCCGCGTGAAGGCGCGCGTCGATCGTCTGTGGACGGAGATCGGCCTATCGTGA

296. Burkholderia pseudomallei K96243 (SEQ ID NO. 296)

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297. Bordetella parapertussis (SEQ ID NO. 297)

TTGAAGTATCGCGACCTCCGAGATTTTCTTGCCCAGCTTGAACGCCAGGGCGAACTCAAACGCATCACCGCGCCG GTCTCGACGCGGCTGGAAATGACCGAGATTGCCGACCGGGTGCTGCCGCCCGGCCCGGCCCTGCTGTTCGAG AACGCCCGCCACAACGACGCCCGGCCGACATGCCGGTGCTGGCCAACCTGTTCGGCACGCCGCGGCGGGTCGCC TGGGGCATGGGGGCCGACGTCGGCGCCCTGCGCGAAACCGGCGAACTGCTGGCCTCCCTGCGCGAGCCCGAA GCGCCCAAGGGCCTGCGCGACGCCTGGCCAAGGTGTCCATGCTGAAAGCCGCCCTGTGGGACATGAGCCCCAAG ACCTGCTGGCCGGCGATGTGGCGCCCCTGCTCGCCTGGGGGCCTGATCACGCGCGGGCCGAACGCCCGGCGG GGCGCGCTGGACTTCCGCGACCACGCCCAGGCCCACCCGGGCAAGTCGTTTCCCATCGCCGTGGCGCTGGGTGCC GACCCGGCCACCATCCTGGACGCGGTCACGCCGGTGCCGGACACGCTGTCCGAATACCAGTTCGCCGGGCTGCTG $\tt CGCGGCTCGCGAGGTCGTCAAGGCGCTGGGCAGCTGTCGGTGCCGGCCTCGGCCGAGATCGTGCTC$ GAGGGCCACCTGCTGCCGGCCGACGATCCGCGCGCGCCGTCGCTGCCGCGGTGCCCGAGGGCGCCAACCCGCCCCCG GCCACCGGCTACGAAATGGCCCTCGAAGGCCCCTATGGCGACCATACCGGCTACTACAACGAGCAGGACTGGTTC CCGGTGTTCACGGTGGACCGCATCACCATGCGGCGCAACCCCATCTACCACCTATACCGGCAAGCCGCCC GACGAGCCGGCCGTGCTGGGCGTGGCGCTGAACGAGGTATTCGTGCCGCTGCTGCGCCGCCAGCTGCCCGAAATC GTCGATTCTACCTGCCCCGGAAGGCTGCAGCTACCGCCTGGCGGTGGTGTCGATCCGCAAGCAGTACGCCGGC CACGCCAAGCGCGTGATGTTCGGCCTGTGGAGCGTGCTGCGGCAGTTCATGTACACCAAGTTCATCGTGGTGGTC GACGAAGACATCGACCCGCGCGCACTGGACCGAAGTGGTCTGGGCCATGACCACGCGCATGGACCCCGTGCGCGAC ACGGTGCTGGTCGAGAACACGCCGATCGATTACCTCGATTTCGCCTCGCCGGTGTCCGGCCTGGGCGGCAAGATG GGGCTGGACGCCACCAACAGTGGCCGGGCGAAACCAGCCGCGAATGGGGCACGCCCATACACATGGACGAGGCG GTCAAGCGCCGGGTGGATGCCATGTGGGACACGCTGGGACTGTAG

298. Bordetella bronchiseptica RB50 (SEQ ID NO. 298)

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TGGGGCATGGGGGCCGACGACGTCGGCGCCCTGCGCGAAACCGGCGAACTGCTGGCCTCCCTGCGCGAGCCCGAA GCGCCCAAGGGCCTGCGCGACGCCGCTGGCCAAGGTGTCCATGCTGAAAGCCGCCCTGTGGGACATGAGCCCCAAG ACCGTGCGCAGCGCCTGCCAGGAAATCGTCTGGGAAGGCGCCGACGTCGACCTGGGCCGCCTGCCCATCCAG ACCTGCTGGCCGGGCGATGTGGCGCCCCTGCTCGCCTGGGGCCTGGTGATCACGCCGGGGCCGAACGCCCGGCGG GGCGCGCTGGACTTCCGCGACCACGCCCAGGCCCACCCGGGCAAGCCGTTTCCCATCGCCGTGGCGCTGGGTGCC GACCCGGCCACCATCCTGGGCGCGGTCACGCCGGTGCCGGACACGCTGTCCGAATACCAGTTCGCCGGGCTGCTG $\tt CGCGGCTCGCGAGGTCGTCAAGGCGCTGGGCAGCTGTCGGTGCCGGCCTCGGCCGAGATCGTGCTC$ GCCACCGGCTACGAAATGGCCCTCGAAGGCCCCTATGGCGACCATACCGGCTACTACAACGAGCAGGACTGGTTC CCGGTGTTCACGGTGGACCGCATCACCATGCGGCGCAACCCCATCTACCACCTATACCGGCAAGCCGCCC GACGAGCCGGCCGTGCTGGCGTGGCGCTGAACGAGGTATTCGTGCCGCTGCTGCCGCCAGCTGCCCGAAATC GTCGATTTCTACCTGCCCCGGAAGGCTGCAGCTACCGCCTGGCGGTGTGTCGATCCGCAAGCAGTACGCCGGC CACGCCAAGCGCGTGATGTTCGGCCTGTGGAGCGTGCTGCGGCAGTTCATGTACACCAAGTTCATCGTGGTGGTC GACGAAGACATCGACCCGCGCGCGACTGGACCGAAGTGGTCTGGGCCATGACCACGCGCATGGACCCCGTGCGCGAC ACGGTGCTGGTCGAGAACACGCCGATCGATTACCTCGATTTCGCCTCGCCGGTGTCCGGCCTGGGCGGCAAGATG GGGCTGGACGCCAACAAGTGGCCGGGCGAAACCAGCCGCGAATGGGGCACGCCCATACACATGGACGAGGCG GTCAAGCGCCGGGTGGATGCCATGTGGGACACGCTGGGACTGTAG

299. Bordetella pertussis Tohama I (SEQ ID NO. 299)

TTGCCGGGATCTGCCTTGAAGTACCGCGACCTCCGAGATTTTCTTGCCCAGCTCGAACGCCAGGGCGAACTCAAA CGCATCACCGCGCCGGTCTCGACGCGGCTGGAAATGACCGAGATTGCCGACCGGGTGCTGCGCGCCGGCGGCCCG CCGCGGCGGGTCGCCTGGGGCATGGGGGCCGACGACGTCGGCGCCCTGCGCGAAACCGGCGAACTGCTGGCCTCC CTGCGCGAGCCCGAAGCGCCCAAGGGCCTGCGCGAGGTGTCCATGCTGAAAGCCGCCTGTGG GACATGAGCCCCAAGACCGTGCGCAGCGCCCTGCCAGGAAATCGTCTGGGAAGGCGCCGACGTCGAGCTGAGC CGCCTGCCCATCCAGACCTGCCGGGCGACGTGGCGCCCCTGCTCGCCTGGGGCCTGGTGATCACGCGCGGG CCGAACGCCGGCGGCAGAACCTGGGCATCTACCGCCAGCAGCCGCTGGGGCCGAACAAGCTGATCATGCGCTGG CTGTCGCACCGGGGCGCGCGCTGGACTTCCGCGACCACGCCCACGCCCACCCGGGCAAGCCGTTTCCCATCACC GTGGCGCTGGGCGCCGCCACCATCCTGGGCGCGGTCACGCCGGTGCCGGACACGCTGTCCGAATACCAG TTCGCCGGGCTGCTGCGCGCTCGCGCACCGAGGTCGTCAAGGCGCTGGGCAGCGACCTGTCGGTGCCGGCCTCG GCCAACCCGCCCCGGCCACCGGCTACGAAATGGCGCTCGAAGGCCCCTATGGCGACCATACCGGCTACTACAAC GAGCAGGACTGGTTCCCGGTGTTCACGGTGGACCGCATCACCATGCGGCGCAACCCCATCTACCACCTAT ACCGGCAAGCCGCCGACGACGCCGCCGTGCTGGGCGTGCGCGCTGAACGAGGTATTCGTGCCGCTGCTGCCGCCGC CAGCTGCCCGAGATCGTCGATTTCTACCTGCCCCCGGAAGGCTGCAGCTACCGCCTGGCGGTGGTGTCGATCCGC AAGCAGTACGCCGGCCACGCCAAGCGCGTGATGTTCGGCCTGTGGAGCGTGCTGCGGCAGTTCATGTACACCAAG TTCATCGTGGTGGTCGACGAAGACATCGACCCGCGCGACTGGACCGAAGTGGTCTGGGCCATGACCACGCGCATG GACCCCGTGCGCACACGGTGCTGGTCGAGAACGCGCCTATCGATTACCTGGATTTCGCCTCGCCGGTGTCCGGC

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 $\tt CTGGGCGGCAAGATGGGCCGCCACCAACAAGTGGCCGGGCGAAACCAGCCGCGAATGGGGCACGCCCATACACATGGACGAAGCGGTCAAGCGCCGGGTGGATGCCATGTGGGACACGCTGGGACTGTAG$

300. Legionella pneumophila subsp. pneumophila str. Philadelphia 1 (SEQ ID NO. 300)

ATGAAGTATTCAGATCTGAGAGATTTCATAGCCCAACTTGAATCACGTGAATTATTAAAACGTATTGATTATCCT GTATCACCTCATCTTGAGATGACCCTAGTCAGCGATAAAGTGTTGCGCTCAGGAGGGCCAGCCCTTCTGTTTACC AATACCCCCAATTACAACATGCCTGTACTGACCAATCTTTTTGGTACGGTAGAGCGCGTGGCTTTGGGAATGGGT GAGGAATCAATAGTGGCTTTGAGGGAGATTGGAAAATTATTGGCTGCTTTAAAGGAGCCCGATCCTCCCAAAGGC TTCAAAGACGCTTTTTAGCAAGTTGCCCTTATTGAAACAAGCGCTGAATATGGCACCCAAATATGTCAGTGGAGCC GAGTGCCAGACTCATGTGTGGGGAAAAGGATGAAGTGGATTTAACCTTATTGCCCATCCAAACGTGTTGGCCCGGA GATGTTGCTCCTCTAATTACCTGGGGTTTGGTTACTACTCGTGGCCCACACCAGTCCAGAGAAAACATGGGCATC TATCGCCAGCAACTATTAAGTAAAAACAAATTGATCATGCGCTGGTTATCTCACCGCGGAGGTGCTTTGGATTAC CAGGCCTGGCAACAAGAATATCCCAAAGAGCGTTTCCCTGTTGCGGTGACTTTAGGCGCTGATCCAGCCACCATA CCAGGAAATGAGGCCCCGAAGGGCCTTATGGCGATCACACCGGTTATTATAATGAAGTCCAATCTTTTCCTGTT TTTACGGTAGAGCGTATTACTCATCGCGATAAACCTATTTACCACAGTACTTATACCGGAAGACCGCCAGATGAG CCAGCCATTTTGGGAGTTGCCTTAAATGAAGTGTTCATTCCCTTGTTACAAAAACAATTCCCAGAGATTGTGGAT TTTTATTTGCCGCCAGAAGGATGCTCTTATCGTTTGGCTGTAGTCACTATAAAAAAGCAATATCCAGGACATGCT AAACGTATTATGATGGCTGTTTGGTCTTTCTTGCGCCAGTTTATGTATACCAAGTTCGTCATTGTTTTGTGATGAT GATGTGGACGCGCGCAATTGGCAAGATGTCATATGGGCAATGACCACGCATGGATCCGTCCCGCGATACAGTC ATGGTAGAAAATACACCCATTGATTATCTGGACTTCGCTTCCCCAGTTTCAGGATTGGGTTCCAAGATGGGTATG AATAGAGTAAATGGTTATTGGTCCTTATTAGGATTAAAATAA

301. Klebsiella pneumoniae ATCC 13883 (SEQ ID NO. 301)

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302. Serratia liquefasciens ATCC 27592 (SEQ ID NO. 302)

303. Brucella melitensis (SEQ ID NO. 303)

CCCGAAGCACCCGAAACACCGATGACGATCCGCTTCATATCCGTTTGTCCCTGTCGAGGCCGAGTTCATCCCAGA TCGCGTCCACACGGGCGATGGTTTCTTCATTCATGGCCAGAACCTTGCCCCATTCGCGGTCCGTTTCAGGACCGA $\verb|TCTTGTTGGTGGCGTCAAGACCGAGCTTTCCGCCAAGGCCGGAGCGTGGCGAGGCGAAATCCAGATAATCGACCG|\\$ GCGTGTCGGAAAGTGTCACCACGTCGCGGCTTGCATCAAAGCGGGTGGCAAGCGCCCACATCACATCGTCCCAGT TGTGTACATCGATATCGGGATCGACGGCGATAATGAGCTTGGTATAGCTGAACTGCGGCAGCATGGACCAAAGCC CCATCATCACGCGCCGCCTGCCCCGGATAACGCTTGTCGATGGAAACCACCATGGCGCGGTAGGAACAGGCGG $\tt CAGGCGGCAGCCAGAGATCGGCTATCTCGGGAAACTGCTTGCGCACGGCACGGCACGAAAAGCTGGTTCATCACCT$ CGCCAAGCCGCGAAGGCTCGTCCGGCGGCGCCTCCGTATAGGTGGAAAGATAGACCGGCTTCTTGCGCATGGTGA TCGCCGTCACCTGCATGACGGGAAACGCCTCCACGCTGTTATAATAGCCGGTATGGTCCCCATAAGGCCCTTCGG GCGCGGTTTGTGTAGCGGAAACCCGACCTTCAAGAACGATTTCTGCATTGGCGGGCACCATCAGCGGCACCGTGC GCATAACTGCGGCCAGAATGGTCGCCGGGTCAACGCCGATGGCAATTGCAACCGGCATGTCCTCACCGCGCTTTT GCCACATGCGATGGTGGCGCGCGCCGCCGATGCGCGAGCCCATGATAAGCCGGTTCTCTCCCAGTTTCT GCATCCGGTAAATGCCGACATTGACATCGGAGGGATCGTCCGGCGCGCGTGTGATAACGAGCGGCCAGGTGATGA GCGGCGCAGGCTCGCCCGGCCAGCACTTGGATCGGCAGCGTGTCGAGATTGACCGATGCGCCTTCCATCACAA GGCCATGAACCGGCGCCCGGCTCACCTGGCGGGGGGCGCATGTTGAGGGCTGCCTTGGCCATCGGCAGCTTTTCCC ATATTTCACCGGCCGAACGCGGCTTCGGCGCACGCAATTCGGCCAGCATTTCAGCCAGAAGCGGCAATTCCT CCGGCAGACGCCCAAGCCCCCAGGCGATACGCCGCTCGGACCCGA

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Figure 13. Molecular marker VIII (hypothetical protein yleA) in Gram-negative bacteria (SEQ ID NOs 304-325).

304. Haemophilus influenzae (SEQ ID NO. 304)

TTAGCCGTGATAACGCCCTACGCCTAATTCATCTTCTTTACGTGTGCGATTCATCATCTTCTTGTGGAGATTGCGC AATACGTAATCCCATTTCATCTTCAGTACGCACCACTTCGCCACGTAACGAATTAGTATAAACATCAGTGATTTT CACATCCACAAACTTACCGATCATTTCTGGAGAACCTTGGAAATTAACAATACGATTCGTTTCAGTACGTCCCGT CAATTCCATAATATCTTTCTTCGATGGGCCTTCAACTAACACGCGCTGCTCTGTGCCAAGCATACGACGGCTAAA TTGTGCCGCTTGTTGATTAATACGCTCTTGTAGCACATAAAGACGCTGTTTCTTTTCATCTTCCGTGACATCATC TGGCATATCTGCTGCTGGCGTACCTGGTCGGGCTGAGTACACAAAACTGAAGCTCATATCAAAGTTTACTTGTGC AATCAAATTCATAGTTTGCTCAAAATCTTCCGCCGTTTCACCAGGGAAACCAACAATAAAGTCAGAGCTGATTTG AATATCTGGGCGCACAGCACGAAGTTTACGAATAATGGATTTATATTCTAATGCGGTATGAGCACGTTTCATCAT TGTTAATACACGGTCAGAACCTGCTTGCACTGGAAGATGTAAGAAACTCACTAATTCAGGCGTATCACGATACAC ATCAATAATATCATCGGTAAATTCTATTGGATGACTGGTTGTGAAACGTAAACGGTCAATACCATCAATTGATGC GACAAGACGAAGCAACTCAGCAAAGCTGCAAATTTGACCATCATGCGTTGGCCCACGATAAGCATTTACATTTTG ACCAAGTAGATTGACCTCACGCACACCTTGTTCCGCAAGTTGCGCAATTTCAAATAGCACATCATCTACAGGACG AAATGCCGTTGGGCCTTCTGCGCGAGGTTCTGGTAAGCGGTCAAATTTCTCAATTTCAGGGAAACTTACGTCTAC GACGGAACTTTTTCCACCACGAATTTGATTAATCATTTCAGGCAAGCGATGCAAAGTTTGCGGGCCAAAAATAAT ATCCACATAAGGCGCACGATGGCGAATATGTTCCCCTTCTTGAGAGGCTACACAGCCGCCCACACCAATCACTAA ATTTGGATTATTTTCTTTAATTCTTTCCAACGCCCAAGTTGGTGGAACACTTTTTCTTGTGCTTTTTCACGAAT AGAACAGGTATTTAATAATAATACGTCTGCTTCTTCAGGTGCTTCCGTGAGTTCTAATCCGTGGGTGCTTAATAA AAGATCAGCCATTTTAGATGAATCATATTCATTCATCTGGCAGCCCCAAGTTTTAATATGTAATTTTTTGAGTCAT

305. Pasteurella multocida (SEQ ID NO. 305)

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ATCGACATAAGGAGCACGAGTACGAATGTGTTCTCCTTCTTGTGAGGCAACACAGCCCCCAACACCGATAACGAG
TCCCGGCTTATGTTCTTTAATTCTTTCCAACGTCCTAATTGATGGAAAACTTTTTCTTGTGCTTTTTCACGAAT
TGAGCAAGTGTTTAACAATAACACATCCGCTTCTTCCGGAATTTCTGTTAACTCTAAGCCGTGAGTACTGTTTAA
GAGATCTGCCATTTTAGATGAATCATATTCATTCATCTGACAACCCCACGTTTTAATATGTAATTTTTTGCGTCAT

306. Haemophilus ducrei (SEQ ID NO. 306)

TTACAGATTTACTGCGTATTTGCCTACACCTAAATCATCTTCCTTACGGGTCCGTGCAATGACACTTGATGCTGA TTCAACAATACGTAAACCCATTTGATCTTCTGTTCTGATCACTTCACCGCGTAATGAGTTTGAGTAAACATCGGT GATTTTAATATCTACGAATTTGCCGATCATATTTGGTGTGCCGATGAAATTAACTACACGATTGGTTTCTGTACG ACCCGTTAATTCCATAATATCTTTTTTAGATGGGCCTTCAACCAAAATTCGTTGTTCAGTGCCAAGCATTAAGCG ACTAAATTGCATCGCTTGATGGTTAATTCGTTGTTGTAAGTGTGCTAAGCGGTCTTTTTTCTCATTTTCAGACAC ATCATCAGGTAAGTCTGATGCAGGCGTACCTGGACGCGCAGAGTAGATAAAGCTAAAGCTCATATCAAAATTGAC TTGTTCAATATTTTCATTGTTTGTTCAAAGTCTTCCGCTGTTTCGCCAGGAAAGCCAACAATGAAATCTGAGCT AATTTGGATATTTGGACGAACCGCACGTAATTTACGAATAATGGCTTTGTATTCTAATGCGGTGTGGTTACGTTT CATCATGGTTAAAACACGATCGGCGCCACTTTGGATAGGTAAATGCAAGAAGCTGACCAATTCTGGAGTATCACG ATACACTTCAATAATGTCGTCGGTGAATTCAATGGGGTGGCTTGTGGTATAACGTAAGCGGTCAATACCATCAAT GGCGGCAACTAAACGTAATAATTCTGCAAAAGTGCAAATGCCACCATCAAAGGTTTCACCACGGTAAGCATTAAC GTTTTGACCCAGCAAGTTAACTTCACGAACGCCTTGCTCTGCTAATTGTGCGATTTCGAATAAGACATCATCAAC TGATACGAAAGCAGTTGGACCTTCTGCTTTGGGTTCTGGTAAGCGGTCGAATTTTTCAATTTCTGGGAAGGAGAT ATCGACTACTGCACGATCGCCTGATCGGATCTGGTTGATCATTTCTGGTAAGCGGTGCAATGTTTGTGGCCCAAA TACTATATCAACAAAAGGGGCACGTTCACGGATATGTTCACCTTCTTGTGAAGCAACACACGCCAACGCCAAT AATTAAATCGGGTTTGTCCTTTTTCCAGTTTTTCCAACGACCAAGTTGTGAAAAGACTTTTTCTTGTGCTTTTTC ACGAATTGAGCAAGTATTCAATAATAAAATATCCGCTTCTTCAGGTTTATCGGTTAATTCTAATCCGTGTGTTGA CAT

307. Vibrio parahaemolyticus (SEQ ID NO. 307)

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ACTAACTTCTTCACCACGAGTGTATGGTACAACGCAGTAAGTGCAGTATTTTGAACAGCCTTCCATGATAGAAAC
AAACGCCGTCGCACCTTCTGCACGTGGCTCAGGTAGGCGGTCGAACTTTTCAATCTCTGGGAACGAAATGTCCAT
TACCGGTGCATCGTCAGGTTTGAGATTGTTTGATCATCTCAGGTAGGCGGTGCAGAGTTTGAGGGCCAAAGATCAC
GTCAACGTATGGTGCACGCTCACGGATGTGGTCACCTTCTTGTGTTGCTACACAACCACCTACACCGATAACTAC
GCCAGGTTTTTTATCTTTTAGTGTTTTCCAACGGCCTAGCTGGTGGAAAACTTTCTCTTGCGCTTTTTCACGGAT
CGAACAGGTGTTAAGTAGAAGTACGTCTGCTTCCTCTGGCTCTTCCGTCAGCTCATAGCCGTTTGCAGCATTAAG
CAGGTCGGCCATTTTTGATGAATCGTATTCGTTCATCTGGCAGCCCCAGGTTTTAATTAGCAGTTTCTTACTCAT

308. Yersinia pestis (SEQ ID NO. 308)

GAATTTACCAATCATGTCGGGTGAACCCTCAAAGTTCACGACGCGGTTGTTTTCCGTACGCCCGGCCAGTTCCAT GACATTTTTGCGAGAGGTACCCTCCACCAAAACACGCTGTACTGTCCCTACCATCTTACGGCTAATTTCCATCGC CTGTTGGCTAATGCGTTGTTGCAGGATATGTAGCCGCTGTTTTTTCTCCTCTTCGGACACATTGTTGGGTAAATC AGCCGCTGGTGTGCCGGGACGCGGGGAGTAAATAAAGCTGTAGCTGGTATCAAAATGAATATCTGCGACCAGTTT CATGGTCTGTTCAAAATCCTGCTGGGTTTCACCAGGGAAGCCGACAATAAAATCAGAACTTATCTGGATATCAGG GCGTGCTTGACGCAGTTTGCGGATGATGGCTTTGTATTCCAAGGCGGTATGGGCACGCTTCATCATGGTCAAAAT ACGGTCAGAACCGCTTTGTACCGGCAAATGCAGGAAGCTCACCAATTCAGGCGTATCGCGATAAACATCAATGAT ATCGTCAGTAAACTCAATGGGGTGGCTGGTGGTAAATCGTACCCTATCGATACCATCAATCGCCGCAACCAAACG CAACAGCTCGGCAAAACTACAGATATCGCCATCGTAGGTTGCCCCGCGGTAGGCGTTAACATTCTGGCCGAGTAA GTTGACTTCACGTACGCCTTGAGCGGCTAACTGGGCGATTTCAAAAAGAATGTCATCGCTTGGACGGCTGACTTC TGGGCCTTCAGCCCGTGGTTCTGGCAAACGGTCAAATTTTTCAATTTCGGGAAAACTGATATCCACGACAGGGCT ATTCGTTCCTTGCACGTGGTTAATCATTTCCGGTAAACGATGCAGCGTTTGTGGCCCGAAGATGACATCGACACA GGGGGCGCGCTGGCGCAATTGTTCACCTTCCTGTGACGCCACGCAACCACCGACCCCAATAATCAACTGCGGGTT TTTCTCTTTCAATAATTTCCATTGCCCTAGCAGGCTGAATACTTTTTCCTGTGCTTTTTCCCGGATAGAACAGGT ATTTAGCAGCAGTAAATCCGCTTCTTCCGGGATGGTGGTTAACTGGTAGCCATGGGTACTGGCCAAGAGATCTGC CATTTTAGATGAATCGTATTCATCATCTGGCAACCCCAGGTTTTGATATGCAGTTTTTTAGTCATCGGGTTATT CATCATCAAAATCACCTCGTTCCGTGCGGTACTCCGTTGTGGTAGATAATCTCCGTTGTAGTAGAGAGTCGCAAA GGCTTCGTCGTTAGGGAGCATTGTAGTCATTTGCCTCTGCGATGACCACCGCAGAACCGTTGAGTTATTCTGTTG AGTGATAAAAAATCCGTTACACTGCGGTTAGACAAAACCTTGCTAATG

309. Vibrio cholerae (SEQ ID NO. 309)

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310. Escherichia coli souche K12 (SEQ ID NO. 310)

TTACGGCTGATAATAACCCACGCCAAGGTCGTTTTCTTTGCGGGTACGGGCAATCACTGATTCCGGTGTTTCTGC CACGCGCAGACCCATTTCATCTTCAGTACGCACCACTTTACCGCGCAGAGAGTTCGGGTAGACGTCGGTAATTTC TACATCGACGAATTTACCGATCATATCCGGCGTGCCTTCGAAGTTGACCACGCGGTTATTTTCCGTACGCCCGGA AAGCTCCATGATGCTCTTACGCGATGTACCTTCTACCAGAATACGCTGGGTGGTGCCGAGCATCCGGCGGCTCCA CGCCATCGCTTGCTGATTAATGCGCTCTTTGCAGAATATACAGACGCTGCTTCTTCTTCTTCTTCCGGAACATCATC AACCATATCGGCGGCTGGTGTACCCGGACGTGCAGAGATAAAGCTGTAGCTCATGTCGAAATTGACGTCGGC AATCAGCTTCATCGTTTTCTCGAAGTCTTCGGTGGTTTCGCCAGGGAAGCCAACGATGAAATCAGAACTGATCTG AATATCTGGACGCCGCACGCAGTTTACGGATGATCGCTTTGTACTCCAGCGCCGTATGGGTACGGCCCATCAG GTTCAGAATGCGATCGGAACCGCTCTGTACCGGCAGATGCAGGAAGCTCACCAGCTCCGGCGTGTCGCGATACAC ACCAGACGCAGCAGATCGGCAAACGATCCGGTGGTGCCGTCGTAGTTTTCACCACGCCAGGCGTTCACGTTCTGA AACGCGGTCGGCCCTTCGGCGCGCGGTTCCGGTAGACGGTCAAACTTCTCGATTTCCGGGAAGCTGATATCTACA ACCGGGCTGCGGTCGCCACGCACGTGATCATCTCCCGCAGACGGTGCAGCGTTTGCGGCCCAAAAATAATA ${\tt TCGACATAGTGGGCGCGCTGGCGAATGTGCTCGCCTTCTTGCGATGCCACGCAGCCACCGACGCCGATAATCAGG}$ TCTGGATTCTTCTCTTTTAACAGTTTCCAGCGACCCAACTGATGGAAGACTTTTTCCTGAGCCTTCTCGCGGATT AGATCGGCCATCTTCGATGAATCGTACTCGTTCATCTGACAGCCCCAGGTTTTAATATGGAGTTTTTTGGTCAT

311. Escherichia coli souche 0157:H7 (SEQ ID NO. 311)

TTACGGCTGATAATAACCCACGCCAAGGTCGTTTTCTTTGCGAGTACGGGCAATCACCGATTCTGGTGTTTCTGC
CACGCGCAGACCCATTTCATCTTCAGTACGCACCACTTTACCGCGCAGAGAGTTCGGGTAGACGTCGGTAATTTC
TACATCGACGAATTTACCGATCATATCCGGCGTGCCTTCGAAGTTGACCACGCGGGTTATTTTCCGTACGCCCGGA
AAGCTCCATGATGCTCTTACGCGATGTACCTTCTACCAGAATACGCTGGGTGGTGCCGAGCATCCGGCGGYTCCA
CGCCATCGCTTGCTGATTGATACGTTCTTGCAGAATATACAGACGCTGCTTCTTCTCTTCTTCTTCTCCGGAACATCATC
AACCATATCGGCGGCTGGTGTACCCGGACGTGCAGAGAAGATAAAGCTGTAGCTCATGTCGAAATTGACGTCGGC
AATCAGCTTCATCGTTTTCTCGAAGTCTTCGGTGGTTTCGCCAGGGAAGCCGACGATGAAGTCAGAACTGATCTG
AATATCTGGACGCCGCCGCACGCAGTTTACGGATGATCGCTTTTGTACTCCAGCGCCGTATGGGTACGTCCCATCAG
GTTCAGAATGCGATCGGAACCGCTCTGTACCGGCAGATGCAGAACCTCACCAGCTCCGGCGTGTCGCGATACAC

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312. Pseudomonas aeruginosa (SEQ ID NO. 312)

CCGCCGTACGGTCGTCGGCCTCAATGCAGGGTGCTGTCGATCAGGGTACCGCGCAGCGAGTGCGCAGCGCGTCG TCGATGTGCACCTGGGCGAACTGGCCGATCAGGCGTGGATTGTCGCAGCGGAAGTTGACGATCCGGTTGTTCTCG GTGCGCCCCTGGAGCATGCCTGGGTCCTTCTTCGAGAAGTCGGTGACCAGGATCCGCTGGGTGCTGCCGACCATG $\tt CGCCGGCTGATCTCGTAGCCTTGCTGGTGGATGCGGCTCTGGAGGATCTGCAGGCGCTGTTTCTTCACTTCTTCC$ CCGACGTCCTCCACCAGCTTCATGGTCTGCTCGAAGTCCTTCTCGGTTTCGCCGGGGAAACCGACGATGAAGTCG GAGCTGATGCAGATGTCCGGGTACCGCGGCCTTCAGCTTGCGGATACGCGACTTGTATTCCAGCACGGTATGGTTG CGCTTCATCGCCGCCAGCACGGGTCGGAGCCCGACTGCACCGGCAGGTGGATGAATTTCACCAGCTCCGGCACC TCGGCGTGGGCCTGGATCAGCGCGTCGGAGAATTCCAGCGGGTGCGAGGTGGTATAGCGGATGCGCTCGATACCG TCGACGGCGGCGACCACCCGCAGCAGTTCGGCGAAGTCGGCCAGGCGGCCATCGTGGGTCAGGCCGCGGAAGCCG TTGACGTTCTGTCCCAGCAGGGTGACTTCGCGGACGCCGTTCTCGGCCAGGTGGATCACTTCGGCGATCACGTCG TCGAATGGTCGGCTGACTTCCTCGCCGCGGGTGTAGGGCACCACGCAGAAGCTGCAGTACTTGCTGCAGCCTTCC ATCACCGAGACGAAGGCGGTGGGGCCATCGACCCGCGGTTCCGGCAGGCGGTCGAATTTCTCGATTTCCGGGAAG GACACGTCGACCTGCGGCTTGCGCGTGCTGCGCGCGTCGATCATTTCCGGCAGGCGGTGCAGGGTCTGCGGG $\tt CCGATCACCAGGTCGGGATTCTGCTGCTTCAGCTCGCGCCACATGCCGAGCTTGGAAAACACCTTTTCCTGGGCC$ TTCTCGCGGATCGAGCAGGTATTGAGCAGGATGACGTCGGCCTCGGCGGCGTTTTCGGTCACCTCGAGGGCTTGG TGTTCACCGAGCAGGTCCGCCATTCGCGACGAGTCGTACTCGTTCATCTGGCAGCCGTGGGTTTCGATGAAAAGC GTTGCTGGCCGAAAGGCTGTGCTATGATTCGCGCCCTTCATTTTCCGGCATTGCTTTCCCCGCCATGAACAAGCG CGAAAACCCCATCTACAAGGTGATTTTCCTCAACCAGGGCCAGGTCTTCGAGATGTATGC

313. Bordetella pertussis (SEQ ID NO. 313)

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314. Bordetella parapertussis (SEQ ID NO. 314)

GACGACGTCGACCATGTGGCCGATCAGGCCGCGCACGCCGGGAAAGTTGACGATACGGTTGTTCTCGGTACGGCC GATGGCCGCGGCCTGCTGATGAGCGCCTGCAACTGCTGCAGGCGCGCAGCTTGACGTCCTGCGGCGTGTC CTCGATCAGCTTCATGGTCTTCTGGAAGTCCTCCTCGGTCTCGCCCGGGAAACCGACGATGAAGTCCGAGGACAG CGTCAGGCTGGGGCGCGCGCGCGCGCGCGCGCCACCACGGACTTGAACTCCAGCGCGGTGTAGCCGCGCTTCAT GGCCGCCAGCACCCGGTCGCTGCCGGCCTGCACCGGCAGGTGCAGGAACGACACCAGCTTGGGCAGCCGTGCGTA GGCGTCGACCATGCGCTGGGTCATTTCCTTCGGATGCGAGGTCGTGTAGCGGATCCGTTCGATACCGGGAATCTC GTGCACGTATTCCAGCAGCATGGCGAAATCGGCGATTTCGCCGCTGTCGCCCCATGGCGCCGCGGTAGGCGTTGAC GTTCTGGCCCAGCAGCGTGACTTCCTTGACGCCCTGGTCGGCCAGGTCGGCGATCTCGAGCAGGACGTCGTCGAA GGGCCGCGACACTTCTTCGCCGCGCGTGTAGGGCACCACGCAGAAGCTGCAATACTTGCTGCAGCCTTCCATGAT GGACACGAACGCGGTGGCCCCTCGACGCGCGGGGGGCAGGCCTCGAACTTCTCGATCTCGGGAAAGCTGAT GTCGACCTGGGACACGCCCTGGGCGCGCGCGCGCTTGATCAGGTCGGGCAGCCGGTGCAGGGTCTGCGGGCCGAA CACCACGTCGACATAGGGCGCGCGCTTGACGATGGCCTCGCCCTCGGCTGGCCACGCAGCCGCCCACGCCGAT CACCAGGTTGGGGTTCTGCTTCTTGAGGTGCTGTACCCGGCCCAGGTCGGAGAACACCTTCTCCTGCGCCTTCTC GCGCACGGAACAGGTGTTGAACAGGATGACATCGGCATCCTCGGGGTTGTCGGTCAGCTCCAGGCCCTGGTCGGC GCGCAGCACGTCGGCCATCTTGTCCGAGTCGTACTCGTTCATCTGGCAGCCGAAGGTGCGGATATACAATTTGCC CAGGCCCTGGGCGGTGGCCGCCTGCCGCATCGGACGGCCTCGCCGTTTGACAGTGGTTTCTTG CAT

315. Burkholderia pseudomallei (SEQ ID NO. 315)

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GAGCATCGACTGGCTGATCCTCGCGACGTTCTCCTCGATCGTCGCCTGCAGATGTTGCAGGCGCTTGAGCTTGAG CTCGCGCGGCGTGTCGTCGGCGAGATTCGCGGCCGGCCGTGCCGGGCCGGGCTGTAGATGAACGAGAAGCTCGT GTCGTAGCTCATCTCGTGAACGAGCGCCATCGTCTTGTCGAAGTCGGCGTCGGTCTCGCCGGGGAAACCCACGAT GATGTCCGTGGACAGCGACAGATTCGGGCGGATCGCGCGCAGCTTGCGGATCACCGATTTGTATTCGAGCACGGT $\tt GTAGCCGCGCTTCATCGCCATCAGGATGCGGTCCGAGCCGTGCTGGACGGGCAGGTGCAGATGGTCGACGAGCTT$ $\tt CGGCACCTTCGCGTAGACGTCGAGCAGGCGCTGCGTGAACTCCTTCGGATGCGATGTCGTTAGCGGATCCGCTC$ GCCGCGGTAGGCGTTCACGTTCTGGCCGAGCAGCGTGACTTCGCGCACGCCCTGGTCGGCGAGGCCCGCGACCTC GGTCAAGACGTCGTCGAGCGGGCGCGACACTTCATCGCCGCGCGTGTACGGCACGACGCAGTAGCTGCAGTACTT $\tt CTTCTCCTGCGCCTTTTCTCGCACCGAGCAGGTGTTGAACAGGATGATGTCCGCGTCTTCCGGGGTGTCGGTTTT$ $\tt CTCGAGGCCCTCGGCCGCATTGAGCACGTCGACCATCTTGTCGGAGTCGTACTCGTTCATCTGGCAGCCGAAGGT$ TTTTACGTAAACTTTCTTGGTCAT

316. Vibrio vulnificus (SEQ ID NO. 316)

 ${\tt GCTACGTAGGTCCATATCTTTTCAGTACGTACAATCTCACCACGCAGTGAGTTCGCAAATACATCGGTAATTTT}$ ${\tt CACATCAACGAACTGACCAATCAGATCTGCGCTACCTTCAAAGTTTACTACACGGTTGTTTTCTGTACGAGCACG}$ ${\tt TAGCTCCATCAAGTTCTTCTTAGAAGGGCCTTCAACCAGTACACGCTGCTCTGTGCCTAGCATGAGGCGAGAGTA}$ ${\tt GATCAGCTTCATGGTGTCTTGGAAATCTTTGTCGCTTTCACCTGGGAAGCCAACAATAAAGTCAGAACTGATTTG}$ AGCGATGATATCATCGGTGAACTCAAGTGGGTGGCTGGTGGTAAAGCGAATACGGTCGATACCATCGATAGACGC AACAAGGCGAAGCAGTTCTGCAAAAGAACAGATTTCACCATCGTGCGTTGGGCCACGGTATGCGTTTACGTTTTG GCCTAGCAGGTTGACTTCGCGAACACCTTGCTCGGCAAGTTGCGCGATTTCGTAAAGCACATCGTCCATTGGGCG ${\tt GAATGCGGTTGCGCCTTCTGCACGTGGTTCTGGCAGACTGTCAAACTTCTCGATTTCTGGGAATGAAATGTCCAT}$ ${\tt CACTGGTGCATCTTCACTTTGTGATTGTTTGATCATTTCAGGAAGACGGTGCAAGGTTTGCGGGCCAAAGATAAC}$ GTCAACAAAAGGTGCACGTTCACGAATGTGATCGCCTTCCTGTGTTGCTACACAACCACCAACACCGATCACGAC ${\tt GCCTGGCTTTTTATCTTTGAGTGTTTTCCAACGGCCAAGCTGGTGGAACACTTTTTCTTGCGCCTTTTCACGGAT}$ $\tt CGAACAGGTGTTAAGTAATAGAACATCTGCTTCTTCTGGTTCTTCTGTCAATTCGTAGCCATTTGCTGCGTTCAG$ CAGATCCGCCATTTTCGATGAATCGTATTCGTTCATCTGGCAACCCCAGGTTTTAATTAGCAGTTTCTTACTCAT

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317. Vibrio fischeri (SEQ ID NO. 317)

 $\tt CTATGGCGTAAAAGTACCTACACCAAGATCATCTTCACGACGTGTCTTTTCCATCATCATCTGCTGGAGTCATAAC$ AACACGTAAACCCATGTCTTTTTCTGTACGAACTAGTTCACCACGCAGTGAGTTCGCAAATACATCTGTGATTTT AACATCAACAAATTGACCAATAAGATCCGCTGAACCTTCAAAGTTTACAACACGGTTGTTTTCAGTACGAGCACG AAGTTCCATCAGGTTTTTCTTCGATGGGCCTTCAACTAATACACGTTGCTCAGTGTCTAGCATTAGACGAGAGTA TGGATAATCAGCAGCAGGTGTTCCTGGACGCGCAGAGAAGATGAAACTAAAGCTCATGTCGAAGTCGACATCTTT AATCAGTTTCATTGTATCTTGGAAGTCTTTCGCCGTTTCACCAGGGAAGCCAACAATAAAGTCAGAACTGATTTG AGTTAGAATACGATCAGAACCACTTTGAACAGGTAAGTGTAAGAAACTTACTAGCTCTGGCGTATCTTCGTATAC AGCGATGATGTCATCACCAAACTCTAATGGGTGGCTTGTTGTAAAGCGTAAACGGTCGATACCATCGATAGATGC AACCATACGTAATAATTCAGCAAATGTGCAGATATCACCGTCGTGCATTGGACCACGGTACGCGTTAACGTTTTG ACCCAATAGGTTTACTTCACGTACGCCTTGCTCTGCAAGCTGTGCAATTTCAAATAATACGTCATCAAGAGGACG GAACGCTGTTGCACCTTCTGCTTTTGGTTCAGGAAGGTTATCGAACTTTTCGATCTCTGGGAATGAAATATCCAT TACTGGTTTTTCATTTGATTGAGATTGGCGGATCATTTCAGGTAAACGGTGTAAAGTTTGTGGACCAAAAATTAC GTCAACGTATGGAGCTCGTTGGCGAATATGATCACCTTCTTGAGTTGCAACACCAACCCCAACACCGATCACTAG ATCTGGTTTTTTATCTTTTAGGTTTTTCCAGCGGCCTAATTGGTGAAACACTTTCTCTTGTGCTTTTTCACGAAT AGAGCAGGTATTTAATAGTAGAACGTCAGCTTCTGTTGGTTCTTCTGTTAATTCATAACCATTTGCGGCACCTAA AAGGTCGGCCATTTTAGATGAATCGTATTCGTTCATCTGACAGCCCCAGGTTTTGATCAGCAGTTTCTTAGTCAT

318. Yersinia pseudotuberculosis (SEQ ID NO. 318)

TTAAGGCTGATAAATACCTACACCAATTTCATTTTCTTTACGGGTGCGAGCAATCACCGATTGCGGTGACTCGTG GGTTCGCAGGTCCATCTGATCTTCTGTACGCAGTAAAATGCCGCGCAGTGAACTGGCATAAACGTTAACAATTTC GACATCAACGAATTTACCAATCATGTCGGGTGAACCCTCAAAGTTCACGACGCGGTTGTTTTCCGTACGCCCGGC CAGTTCCATGACATTTTTGCGAGAGGTCCCCTCCACCAAAACACGCTGTACTGTCCCTACCATCTTACGGCTAAT TTCCATCGCCTGTTGGCTAATGCGTTGTTGCAGGATATGTAGCCGCTGTTTTTTCTCCTCTTCCGACACATTGTC GACCAGTTTCATGGTCTGTTCAAAATCCTGCTGGGTTTCACCAGGGAAGCCGACAATAAAATCAGAACTTATCTG GATATCAGGGCGCCTGACGCAGTTTGCGGATGATGGCTTTGTATTCCAGGGCGGTATGGGCACGCTTCATCAT GGTCAAAATACGGTCAGAACCGCTTTGTACCGGCAAATGCAGGAAGCTCACCAATTCAGGCGTATCGCGATAAAC ATCAATGATATCGTCAGTAAACTCAATGGGGTGGCTGGTGATAATCGTATCCTATCGATACCATCAATGGCCGC AACCAAACGCAACAGCTCGGCAAAACTACAGATATCGCCATCGTAGGTTGCCCCGCGGTAGGCGTTAACATTCTG GCCGAGTAAGTTGACTTCACGTACGCCTTGAGCGGCTAACTGGGCGATTTCAAAAAGAATGTCATCGCTTGGACG AAACGCAGTTGGGCCTTCAGCCCGTGGTTCTGGCAAACGGTCAAATTTTTCAATTTCGGGAAAACTGATATCCAC GACAGGGCTATTCGTTCCTTGCACGTGGTTAATCATTTCCGGTAAACGATGCAGCGTTTGTGGCCCGAAGATGAC ATCGACACAGGGGGCGCCTGGCGCAATTGTTCACCTTCCTGTGACGCCACGCAACCACCGACCCCAATAATCAA CTGCGGGTTTTTCTCTTTCAATAATTTCCATTGCCCTAGCAGGCTGAATACTTTTTCCTGTGCTTTTTCCCGGAT

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319. Salmonella enterica subspecies paratyphi A (SEQ ID NO. 319)

TTAAGGCTGGTAGAATCCTACGCCCAGCTCATTTTCTTTACGGGTACGGGCAATGACGGACTCCGGCGTTTCGGC GACGCGCAGCCCCATTTCATCTTCGGTACGCACCACTTTTCCGCGCAGGAGTTCGGATAGACGTCAGTAATTTC CACATCGACAAACTTACCAATCATCTCCGGCGTGCCTTCAAAGTTCACCACCCGATTGTTTTCGGTACGGCCAGA CAGTTCCATAATGTTTTTACGTGACGTGCCTTCCACCAGAATGCGCTGTGTCGTGCCGAGCATACGGCGGCTCCA TGCCATCGCCTGCTGATTGATACGCTCTTGCAGAATATACAGACGCTGCTTTTTCTCTTTCTCTTCCGGTACGTCATC AACCATATCGGCAGCCGGCGTTCCCGGACGCGCAGAGAAGATAAAGCTGTAGCTCATATCAAAGTTGACGTCAGC GATAAGCTTCATGGTTTTTTCGAAATCATCGGTAGTTTCGCCAGGGAATCCGACGATAAAGTCAGAGCTTATCTG AATGTCCGGCCGCGCGCGCGCAGTTTACGGATGATTGCTTTATATTCCAGCGCAGTGTGGGTGCGCCCCATCAG ATTCAACACGCGATCGGAACCGCTCTGTACCGGCAGATGCAGGAAACTGACCAGCTCCGGCGTATCGCGGTACAC CTCGATAATATCGTCGGTGAACTCAATCGGATGGCTGGTGGTAAAGCGAATACGGTCAATGCCGTCGATGGCGGC AACCAGACGCAGCAGATCGGCAAAGGTGCCAGTGGTGCCGTCGTAGTTTTCTCCGCGCCCAGGCGTTAACGTTCTG GCCCAACAGGTTGACCTCACGCACGCCCTGCGCCCCTAACTGGGCGATTTCGAACAGGATATCGTCTGAGGGACG GAAAGCGGTCGGGCCTTCTGCGCGCGGTTCCGGCAAACGGTCGAACTTCTCGATTTCCGGGAAGCTGATATCGAC CACCGGGCTGCGGTCGCCACGCACGAGTTAATCATCTCCGGCAGGCGGTGTGAGGTTTGCGGACCAAAAATAAT GTCGACGTAATGGGCGCGTTGACGAATGTGCTCGCCTTCCTGGGAAGCCACGCAGCCGCCGACGCCGATAATCAG ATCGGGATTTTTCTCTTTTAACAGTCTCCAGCGACCTAATTGATGGAAGACTTTTTCCTGAGCCTTCTCGCGGAT CAGATCGGCCATCTTCGATGAATCGTACTCGTTCATCTGACAGCCCCAGGTTTTAATATGGAGTTTTTTAGTCAT CGACTTGCTCTTGCGAAATAGTGGCTGAAAAGCAGGGCGCAT

320. Salmonella typhimurium (SEQ ID NO. 320)

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321. Shigella flexneri (SEQ ID NO. 321)

TTACGGCTGATAATAACCCACGCCAAGGTCGTTTTCTTTGCGGGTGCGGGCAATCACCGACTCCGGTGTTTCTGC CATGCGCAGACCCATTTCATCTTCAGTTCGCACCACTTTACCGCGCAGAGAGTTCGGGTAGACGTCGGTAATTTC TACATCGACGAATTTACCGATCATATCCGGTGTGCCCTCGAAGTTGACCACGCGGTTATTTTCGGTACGCCCGGA AAGCTCCATGATGCTCTTACGCGAAGTCCCTTCTACCAGAATACGCTGGGTGGTGCCGAGCATCCGACGGCTCCA TGCCATCGCTTGCTGATTGATACGTTCTTGCAGAATATACAGACGCTGCTTCTTCTCTTCTTCCGGAACATCATC AACCATATCGGCGGCAGGCGTTCCTGGACGTGCAGAGAAGATAAAGCTGTAGCTCATGTCGAAATTGACGTCGGC AATCAGCTTCATCGTTTTCTCGAAGTCTTCGGTGGTTTCGCCAGGGAAGCCAACAATGAAGTCAGAACTGATCTG AATATCCGGACGCCGCACGCAGTTTACGGATGATCGCTTTGTACTCCAGCGCCGTATGGGTACGTCCCATCAG GTTCAGAATGCGATCGGAACCGCTCTGTACCGGCAGATGCAGGAAGCTCACCAGCTCAGGCGTGTCGCGGTACAC AACCAGACGCAACAGATCGGCAAACGATCCGGTGGTGCCGTCGTAGTTCTCACCACGCCAGGCATTCACATTCTG AAACGCGGTCGGCCCTTCGGCGCGCGGTTCCGGCAGACGGTCAAACTTCTCGATTTCCGGGAAGCTGATATCTAC AACCGGGCTGCGGTCGCCGCACGGAGTTGATCATCTCCGGCAGACGGTGCAGCGTTTGCGGCCCAAAAATAAT ATCGACATAGTGGGCGCGCTGGCGAATGTGCTCGCCTTCTTGCGATGCCACCGACCCCACCCGACGCCGATAATCAG GTCTGGATTCTTCTCTTTTAACAGTTTCCAGCGACCCAACTGATGGAAGACTTTTTCCTGAGCCTTCTCGCGGAT CAGATCGGCCATCTTCGATGAATCGTACTCGTTCATCTGACAGCCCCAGGTTTTAATATGGAGTTTTTTTGGTCAT

322. Pseudomonas syringae (SEQ ID NO. 322)

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GTAGGGCACCACGCAGAAGGTGCAGTACTTGCTGCAGCCTTCCATCACCGACACGTAAGCACTCGGGCCATCCAC
GCGCGGCTCGGGCAAGTGGTCGAATTTTTCGATCTCGGGGAATGAAACATCGACCTGCGGCAAGCGGGTGATGCG
CGCTGCGTCGATCATTTCCGGCAGGCGGTGCAATGTTTGCGGGCCGAACACCACGTCCACGTAGGGCGCGGGTC
GCGGATGGCCGCGCCTTCCTGGCTGGCAACACAGCCGCCGACGCAATCACCATCTCGGGGTTGGCCAGTTTCAG
CTCACGCCAGCGGCCGAGCTGCGAATAGACCCGGTCTTGCGCACGCTCGCGAATCGAGCAGGTGTTGAGCAGGAT
CACGTCGGCGTCTTCCGCGCGAGCGGTGACTTCCAGAGCCTGATGTTCGCCCAGCAGATCGACCATGCGCGAGCT
GTCGTACTCGTTCATCTGGCAACCGTGGGTTTCGATGTAAAGCTTCTTGGCCAT

323. Burkholderia mallei (SEQ ID NO. 323)

TCAGTGCGTGGCGCGCTCGCCGTGCGCGAGCACGAGCTCGCCGCGCAGCGAGTGCGGATACGCGTGATT GATCTTCACGTCGATCATCTGGCCGATCAGGCGCGGGGTGCGCGGGCGCGCGGGGAAAATTCACGACCCGGTT GTTCTCGGTGCGCCCGCGAGCTCGTTCGGATCCTTGCGCGACGCCCCTCGACGAGGATTCGCTCGACCTTGCC GAGCATCGACTGGCTGATCCTCGCGACGTTCTCCTCGATCGTCGCCTGCAGATGTTGCAGGCGCTTGAGCTTGAG CTCGCGCGCGTGTCGTCGGCGAGATTCGCGGCCGGCCGTGCCGGGCCGCGGGCTGTAGATGAACGAGAAGCTCGT GTCGTAGCTCATCTCGTGAACGAGCGCCATCGTCTTGTCGAAGTCGGCGTCGGTCTCGCCGGGGAAACCCACGAT GATGTCCGTGGACAGCGACAGATTCGGGCGGATCGCGCAGCTTGCGGATCACCGATTTGTATTCGAGCACGGT GTAGCCGCGCTTCATCGCCATCAGGATGCGGTCCGAGCCGTGCTGGACGGGCAGGTGCAGATGGTCGACGAGCTT $\tt CGGCACCTTCGCGTAGACGTCGAGCAGCGCTGCGTGAACTCTTTCGGATGCGATGTCGTGTAGCGGATCCGCTC$ GCCGCGGTAGGCGTTCACGTTCTGGCCGAGCAGCGTGACTTCGCGCACGCCCTGGTCGGCGAGGCCCGCCACCTC GGTCAAGACGTCGTCGAGCGGGCGCGACACTTCATCGCCGCGCGTGTACGGCACGACGCAGTAGCTGCAGTACTT $\tt CTTCTCCTGCGCCTTTTCTCGCACCGAGCAGGTGTTGAACAGGATGATGTCCGCGTCTTCCGGGGTGTCGGTTTT$ CTCGAGGCCCTCGGCCGCATTGAGCACGTCGACCATCTTGTCGGAGTCGTACTCGTTCATCTGGCAGCCGAAGGT TTTTACGTAAACTTTCTTGGTCAT

324. Legionella pneumophila (SEQ ID NO. 324)

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325. Bordetella bronchiseptica (SEQ ID NO. 325)

GACGACGTCGACCATGTGGCCGATCAGGCGCGGCACGCCGGGAAAGTTGACGATACGGTTGTTCTCGGTACGGCC CATCAGCTCGTTGGGGTCGCCGCGAAGGGCCTTCGACCAGCACGCGCTGGCGGTGCCGATCATGCCCTGGGC GATGGCCGCGGCCTGCTGATGAGCGCCTGCAACTGCTGCAGGCGGCGCAGCTTGACGTCCTGCGGCGTGTC $\verb|CTCGATCAGCTTCATGGTCTTCTGGAAGTCCTCCTCGGTCTCGCCCGGGAAACCGACGATGAAGTCCGAGGACAG|\\$ GGCCGCCAGCACCCGGTCGCTGCCCGGCCTGCACCGGCAGGTGCAGGAACGACCAGCTTGGGCAGCCGTGCGTA GGCGTCGACCATGCGCTGGGTCATTTCCTTCGGATGCGAGGTCGTTGTAGCGGATCCGTTCGATACCGGGAATCTC GTGCACGTATTCCAGCAGCATGGCGAAATCGGCGATTTCGCCGCTGTCGCCCATGGCGCCGCGGTAGGCGTTGAC GTTCTGGCCCAGCAGCGTGACTTCCTTGACGCCCTGGTCGGCCAGGTCGGCGACCTCGAGCAGGACGTCGTCGAA GGGCCGCGACACTTCTTCGCCGCGCGTGTAGGGCACCACGCAGAAGCTGCAATACTTGCTGCAGCCTTCCATGAT GTCGACCTGCGACACGCCCTGGGCGCGCGCGCTTGATCAGGTCGGGCAGCCGGTGCAGGGTCTGCGGGCCGAA CACCAGGTTGGGGTTCTTGAGGTGCTGTACCCGGCCCAGGTCGGAGAACACCTTCTCCTGCGCCTTCTC GCGCACGGAACAGGTGTTGAACAGGATGACATCGGCATCCTCGGGGTTGTCGGTCAGCTCCAGGCCCTGGTCGGC GCGCAGCACGTCGGCCATCTTGTCCGAGTCGTACTCGTTCATCTGGCAGCCGAAGGTGCGGATATACAATTTGCC CAGGCCCTGGGCGGTGGCCGGCGTGCCGGCATCGGACGGCTGGCGCCGTCGCGTTTGACAGTGGTTTCTTG CAT

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Figure 14 represents marker I (purA) sequences amplified from different Gram-positive bacteria (SEQ ID NOs 326-359)

326 Enterococcus faecalis (SEQ ID NO. 326)

327 Enterococcus gallinarum (SEQ ID NO. 327)

328 Enterococcus flavescens (SEQ ID NO. 328)

329 Streptococcus agalactiae (SEQ ID NO. 329)

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CAATCTATGAAGAATTACCGGGCTGGTCTGAAGATATTACAGCTTGTCGTAGCTTAGATGATCTTCCAGAAAATG CACGTAATTACGTTCGCCGTGTTGGCGAATTGGTTGGTGTTCGTATTTCTACTTTNCTCAGTAGGNCCAGGTC

330 Streptococcus sanguis (SEQ ID NO. 330)

331 Enterococcus faecium (SEQ ID NO. 331)

332 Enterococcus durans (SEQ ID NO. 332)

333 Streptococcus pyogenes (SEQ ID NO. 333)

CTATTTGAAGGGGCACAAGGGGTTATGCTTGATATTGACCAGGAACGTACCCATTTGTAACGTCTTCAAACCCAG
TTGCTGGTGGTGTAACCATTGGTTCTGGTGTTGGCCCAAATAAAATCAACAAAGTAGTTGGTGTCTGTAAAGCCT
ACACAAGCCGTGTCGGTGATGGGCCATTCCCTACAGAACTCTTTGATGAAGTGGGTGAGCGCATTCGTGAAGTGG
GTCATGAGTACGGGACAACGACCGGCCGTCCACGTCGTGTCGGTTTGATTCGGTTGTCATGCGCCACAGTC
GTCGTGTATCAGGTATTACTAACCTCTCTCTGAATTCAATTGATGTTCTTTCAGGGCTTGATACGGTTAAGATTT
GTGTGGCTTATGACCTTGATGGGAAACGTATTGACTATTACCCAGCAAACCTTGAACAACTCAAACGTTGCAAAC

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334 Streptococcus pneumoniae (SEQ ID NO. 334)

335 Streptococcus oralis (SEQ ID NO. 335)

336 Staphylococcus hominis (SEQ ID NO. 336)

CTCTTTGAAGGAGCGCAAGGAGTTATGTTAGATATCGACCATGGTACATATCCTTTTTGTAACGTCAAGTAATCCT
GTGGCAGGTAATGTGACAGTAGGAACTGGCGTGGGTCCAACCTTCGTATCTAAAGTGATTGGGGTATGTAAATCC
TATACATCTCGTGTAGGTGACGGCCCATTCCCTACTGAATTATTCGACGAAGATGGTCATCATATTAGAGAAGTA
GGTCGTGAATATGGAACGACAACAGGACGTCCTCGTCGTGTAGGTTCGACTCAGTTGTATTACGTCACTCT
CGTCGTGTAAGTGGTATTACAGACTTATCTATTAACTCAATTGACGTTTTAACAGGTTTAGATACGGTTAAAATT
TGTACAGCTTATGAGTTAGATGGTGAAACAATCACAGAATATCCAGCAAACTTAGACCAATTACGTCGTTGTAAA
CCAATTTTCGAAGAGTTACCTGGTTGGACGGAAGCATTACAGGTTGTCGTACATTAGAAGAATTACCTGAAAAC
GCACGTAAATACTTAGAACGTATTTCTGAATTATGTGGCGTTCATATTTCAATCTTCTCAGTAGGTCCAGGCC

337 Bacillus anthracis (SEQ ID NO. 337)

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CCTGTATACGAAGAGCTTCCAGGTTGGACAGAAGATATTACTGGTGTAAGATCATTAGATGAGCTTCCTGAAAAT
GCTCGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAGTTCAATTATCTATGTTCTCAGTAGGGCCAGACC

338 Bacillus cereus (SEQ ID NO. 338)

GACNCGGTACCCGTTCGTTACATCTTCTAACCCAATTGCTGGTGTTAACAGTTGGAACTGGAGTTGGTC
CTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTG
AGCTTCATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGCGAGTATGGAACGACAACTGGTCGTCCACGCC
GCGTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAACGGATCTATCATTAAATT
CTATCGACGTTTTAACAGGTATTCCAACTCTTAAAATTTGTGTAGCTTACAAATACAATGGCGAAGTTATTGATG
AAGTTCCAGCTAACTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGGAAGAAGATA
TTACTGGTGTAAAAATCATTAGATGAACTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAG
GAATTCAAATATCTATGTTCTCAGTAGGTCCCCACCA

339 Bacillus megatherium (SEQ ID NO. 339)

340 Enterococcus casseliflavus (SEQ ID NO. 340)

341 Enterococcus raffinosus (SEQ ID NO. 341)

CTATTTGAAGGTGCTCAAGGCGTTATGCTGGATATTGATCAAGGAACCTATCCATTTGTTACTTCTTCGAACCCA
GTTGCCGGTGGGGTAACTATCGGTAGTGGTGTAGGACCTGCTAAAATCGACAAAGTTGTCGGTGTTTGTAAAGCC
TATACTTCACGCGTAGGTGATGGACCTTTCCCAACTGAATTGTTTGATGAAGTTGGAGATCAGATTCGTGAAGTC
GGTCGTGAATATGGAACGACTACTGGTCGTCCACGTCGTGTGGGCTGTTTGACTCGGTTGTGATGCGTCATTCA
AAACGTGTTTCTGGGATTACGAATCTTTCTTTAAACTCGATTGATGCTCTTGAGCGGTCTGGATACAGTGAAAATT
TGTACAGCGTATGAGCTGGACGGAGAACTAATTTACCATTATCCAGCAAGCCTAAAAGAATTAAATCGTTGTAAG

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 $\tt CCCGTTTATGAAGAACTACCTGGTTGGAGCGAAGATATTACAGGCTGCCGTGATTTAGCTGATCTACCGGAAAAT\\ GCGCGTAATTATGTACGTCGCGTTTCTGAACTTGTGGGTGTGCGTATCTCGACCTTCTCAGTTGGTCCTGGTC\\$

342 Staphylococcus aureus (SEQ ID NO. 342)

343 Staphylococcus epidermidis (SEQ ID NO. 343)

344 Stretpococcus mitis (SEQ ID NO. 344)

345 Streptococcus species (SEQ ID NO. 345)

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 ${\tt GTTGGTCAGAAGACATCACAGGTTGCCGTAGCCTAGATGAACTTCCCGAAAATGCTCGTGACTACGTTCGCCGTG}\\ {\tt TTGGTGAACTCGTTGGTGTTCGCATTTCAACATTCTCAGTTGGCCCC}\\$

346 Streptococcus canis (SEQ ID NO. 346)

347 Streptococcus mutans (SEQ ID NO. 347)

TATGGCTTGCNATTGACCAAGGTAACCTATCCATTTGTAACTTCATCAAATCCAGTTGCAGGTGGCGTTACCATC
GGATCTGGTGTTGGACCAAGTAAAATCAATAAGGTTGTTGGTGTCTGCAAAGCCTATACCAGCCGTGTAGGTGAT
GGTCCTTTCCCCACAGAACTTTTTGACCAAACGGGAGAGCGCATTCGTGAAGTTGGGCATGAATACGGGACAACA
ACAGGGCGTCCGCGTCGAGTTGGTTGGTTTGACTCAGTTGTTATGCGTCACAGCCGCCGTGTATCAGGCATTACC
AATTTATCTCTTAACTGTATTGATGTACTTTCAGGTCTTGATATCGTAAAAATCTGTGTAGCCTATGATTTGGAT
GGAAAACGGATTGATCACTACCCTGCCAGTCTCGAACAACTCAAACGCTGTAAACCTATTTATGAAGAATTGCCG
GGCTGGTCTGAAGATATTACAGGGGTTCGCAGTTTAGAAGATCTTCCTGAAAATGCTCGTAATTATGTCCGCCGT
GTAAGTGAATTAGTTGGTGTTCGTATTTCTACTTTCTCAGTNGTCCCC

348 Streptococcus gordonii (SEQ ID NO. 348)

TAATGCTAGCAATTGACCAAGGTACCTATCCATTTGTAACCTCATCTAATCCAGTTGCTGGTGGTGAACGATCG
GTTCTGGTGTGGGGTCCTAGCAAGATTGACAAAGTAGTGGGTGTTTGTAAAGCCTATACAAGTCGTGTTGGTGATG
GTCCTTTCCCAACAGAGCTTTTCGATGAAGTAGGTGACCGCCATTCGTGAGGTTGGTCATGAGTATGGTACAACAA
CAGGACGTCCGCGTCGAGTTGGTTGGACTCTGTTGTTATGCGCCATAGCCGCCGTGTATCTGGGATTACCA
ATCTTTCGCTTAACTCTATCGATGTTTTGAGCGGTCTGGATACAGTCAAGATCTGTGTAGCCTATGATTTGGATG
GCCAAAGAATCGACCACTATCCAGCTAGTTTGGAACAGCTTAAACGTTGTAAGCCGATTTACGAAGAGCTTCCTG
GATGGTCTGAAGATATTACTGGCGTTCGTAAGTTAGAAGATCTTCCAGAAAATGCTCGCAACTATGTTCGGCGAG
TAAGCGAGTTGGTTGGTTACGTATTTCCACCTTCTCAGTTGGCCCC

349 Bacillus species (SEQ ID NO. 349)

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 ${\tt TTGGACAGAAGATATTACTGGTGTAAAATCATTAGACGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGT}\\ {\tt TTCTGAGTTAACAGGAATTCAATTATCTATGTTCTCAGTNGTCCCC}$

350 Bacillus pumilus (SEQ ID NO. 350)

GTTATGGCTTGCTATTGATCAAGGGACATATCCATTTGTCACGTCATCTAACCCAGTAGCTGGAGGAGTGACGAT
TGGTTCTGGCGTAGGACCAACAAAAATTCAACATGTGGTCGGCGTGTCAAAAGCGTACACAACACGTGTTGGAGA
TGGCCCATTCCCGACAGAACTCCATGATGAAATTGGCGATCAAATCCGTGAGGTTGGCCGTGAATACGGTACAAC
AACTGGACGTCCGCGCCGTGTTGGCTGGTTTGACAGTGTCGTTGTCCGTCATGCTCGACGTGTGAGCGGGATTAC
AGATCTATCTCTTAACTCAATTGATGTACTGACAGGGATTGAAACATTGAAAATCTGTGTCGCTTATAAATTGAA
CGGAGAAATCACAGAGGAATTCCCAGCAAGTCTAAATGAACTAGCGAAAATGTGAGCCTGTCTACGAAGAAATGCC
AGGATGGACAGAGGATATTACAGGCGTGAAGAATTTAAGCGAACTGCCTGAAAATGCCCGTCATTATTTAGAGCG
CATTTCACAATTAACAGGTATTCCACTTTCCATTTTCTCAGTTGNCCCC

351 Enterococcus villorum (SEQ ID NO. 351)

352 Bacillus thuringensis (SEQ ID NO. 352)

CNCGGTACCCGTTCGTTACATCTTCTAACCCGATTGCGGGTGGTGTAACAGTTGGAACTGGAGTTGGCCCT
GCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTTGGTGACGGTCCATTCCCTACTGAA
CTTAATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGGGAACAACAACTGGTCGTCCGCCGC
GTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCGCGTCGTTTAGTGGTTTAACGGATCTATCATTAAATTCT
ATCGACGTTCTAACAGATATTCCAACTCTTAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAA
GTTCCAGCAAACTTAAACATTTTAGCGAAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATT
ACTGGTGTAAAAATCATTAGACGAGCTTCCTGAAAATGCAAGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGA
ATTCAATTATCTATGTTCTCAGTGGCCCCNGGGCCCCA

353 Bacillus mycoides (SEQ ID NO. 353)

GGTNCGTACCCATTCGTTACATCTTCTAACCCGATTGCTGGTGTGTAACAGTTGGAACTGGAGTTGGTCCTGCG

AAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTAGGTGATGGTCCGTTCCCTACTGAGCTT

CATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAATACGGAACAACTGGTCGTCCACGCCGCGTA

GGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTTAGTGGTTTAACAGATCTATCATTAAATTCTATC

GACGTTCTAACAGGTATTCCAACTCTTAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAAGTT

CCAGCAAACTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACT

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GGTGTAAGAGCATTAGACGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATT CAATTATCTATGTTCTCAGTGGNCCCCCGG

354 Bacillus weihennstephanensis (SEQ ID NO. 354)

355 Staphylococcus haemolyticus (SEQ ID NO. 355)

356 Staphylococcus saprophyticus (SEQ ID NO. 356)

GCAAGGTGTGATGTTAGATATCGACCATGGTACATATCCATTCGTTCATCAAGTAACCCAGTTGCAGGTAATGTG
ACTGTCGGTGGCGGTGTAGGTCCAACATTCGTCTCTAAAGTTATCGGTGTGTAAAGCCTATACATCACGTGTC
GGCGATGGTCCATTCCCAACAGAACTATTTGACGAAGATGGGCACCACATCCGTGAAGTAGGTCGTGAATACGGT
ACAACAACAGGACGTCCACGTCGTGTAGGTTGGTTCGACTCAGTTGTATTACGTCATTCTCGTCGTGCAAGTGGT
ATTACAGATTTATCTATTAACTCAATTGATGTATTAACAGGCCTTAAAGAAGTTAAAATCTGTACTGCTTATGAG
TTAGACGGTAAAGAAATTACGGAATACCCAGCTAACTTGAAAGACTTACAACGTTGTAAGCCAATTTTTGAAACA
TTACCAGGTTGGACAGAAGATGTGACAGGTTGTCGTTCATTAGAAGAATTACCTAATAATGCGCGTAGATACTTA
GAACGTATTTCTGAATTATGTGACGTGAAGATTTCAATCTTCTCAGTTGGCCC

357 Bacillus subtilis (SEQ ID NO. 357)

CTCAAGGGGTTATGCTTGATATTGACCAAGGGACATACCCGTTTGTCACTTCATCCAACCCGGTCGCCGGAGGGG
TGACGATCGGTTCAGGCGTAGGCCCGACAAAAATCCAGCACGTCGTCGTCGTTATCTAAAGCGTACACAACCCGTG
TCGGTGACGGTCCTTTCCCGACTGAGCTGAAAGATGAAACCGGGGATCAAATCCGTGAAGTCGGACGCGAATACG
GCACAACGACAGGCCGTCCGCGCCGTGTCGGCTGGTTTGACAGCGTTGTTGTCCGCCATGCCCGCGCGTCACC
GAATCACAGATCTTTCTCTGAACTCAATCGATGTGCTGACTGGCATTGAAACATTGAAAATCTGTGTCGCTTACC
GCTACAAAGGTGAAGTGATTGAAGAATTCCCGGCAAGTCTGAAAGCTCTCGCAGAGTGTGAACCGGTATATGAAG

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 ${\tt AAATGCCTGGCTGGACGGAAGATATCACAGGCGCAAAAACATTAAGCGATCTTCCTGAAAATGCGCGCCATTATCTGGAACGCGTGTCTCANCTGACAGGTATTCCGCTTTCTATTTTCTCAGTAGGTCCAGA}$

358 Listeria monocytogenes (SEQ ID NO. 358)

359 Lactococcus lactis (SEQ ID NO. 359)

TNATGCTTGATATTGACNAGGAACATACCCATTTGTAACTTCTCAAACCCAGTAGCTGGTGGGGTAACGATTGGC
TCTGGTGTGGGGTCCATCAAAAATTTCAAAAGTTGTTGGTGTTTGTAAAGCCTATACTTCACGTGTGGGTGATGGT
CCATTCCCAACAGAACTTTTTGATGAAGTTGGACATCAAATTCGTGAAGTAGGACATGAATATGGAACAACA
GGACGTCCACGTCGTGTTGGTTGGTTTGACTCAGTCGTAATGCGTCATGCAAAACGTGTTTCTGGCTTGACAAAT
CTTAGCTTGAATTCAATTGACGTTCTCTCAGGACTTGAAACAGTAAAAATTTGTGTTGCTTACGAACGTAGTAAT
GGTGAACAAATTACTCATTATCCAGCATCACTTAAGGAATTAGCAGATTGCAAACCAATCTATGAAGAATTGCCA
GGATGGTCTGAAGATATTACTTCATGCCGAACTTTAGAAGAGTTACCAGAAGCTGCTCGTAACTATGTTCGTCGG
GTTGGTGAACTAGTTGGCGTACGTATCTCGACTTTCTCAGTNGTCCCC

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Figure 15 represents marker II (pstI) sequences amplified from Gram-positive bacteria (SEQ ID NOs: 360-395; SEQ ID NOs: 397-399), and some Gram-negative bacteria (SEQ ID NOs 396, 400-403).

SEQ ID NO. 360 Bacillus anthracis

SEQ ID NO. 361 Bacillus cereus

SEQ ID NO. 362 Listeria monocytogenes

SEQ ID NO. 363 Streptococcus pneumoniae

SEQ ID NO. 364 Streptococcus pyogenes

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SEQ ID NO. 365 Streptococcus agalactiae

GAGCAGCTTTGATAACGTTGTTAATCAAACGAAGGATTGATGGATTGTATGGTTGATAGAGGTATGAAACTTGCT
CATTCATACGGTCCGCAGCCATTGTGTATTGGATAAGATCATTAGTACCAATTGAGAAGAAATCAACTTCTTTTG
CAAATTGGTCTGCAAGCATAGCTGCCGCTGGGATTTCAATCATAATACCAACTTCAATGCCTTCAGCTACTGCTA
CACCGTCAGCTAACAAGTTCGCTTTCTCTTCTTCAAATATAGCTTTAGCAGCACGGAATTCTTTAAGCAAAGCAA
CCATTGGGAACATGATGCGTAGCTGTCCATGAACTGAAGCACGAAGAAGTGCTCGGATTTGTGTGCGGAACATTG
CATCACCAGTTTCAGAAATTGAAATACGCAATGCACGGAATCCCAAGAACGGATCNTTTTTCNTA

SEQ ID NO. 366 Streptococcus mutans

SEQ ID NO. 367 Enterococcus flavescens

SEQ ID NO. 368 Staphylococcus aureus

SEQ ID NO. 369 Staphylococcus epidermidis

CTTCTTTATGAGAAGCTTCAATAACTTGTTTAACTAATCGTAAAATTGAAGGATTATATGGTTGATATAAGTATG
AAACTCGTTCAGACATACGGTCAGCAGCTAATGTGTATTGAATTAAGTCATTCGTTCCTATACTAAAGAAATCTA

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SEQ ID NO. 370 Bacillus thuringensis

SEQ ID NO. 371 Staphylococcus hominis

SEQ ID NO. 372 Enterococcus faecium

SEQ ID NO. 373 Clostridium perfringens

CNTGTTTGTGAGCTCCATCTATTGTCATTTTGATTAATCTTAATACAGCTGGATGCATTGGATTGTAAAGGTATG
ATACCTTTTCACTCATTCTGTCAGCAGCTAATGTATATTGTATTAAATCGTTAGTTCCTATTGAGAAGAAATCAA
CATGCTTAGCTAATTCATCAGCATAAACTGCTGCAGCTGGGATTTCAACCATGATACCCCATTGAATTGAATCTG
AGTATGCTATACCTTCTGCTTTTAACTCAGCTTTGCATTCTTCAACAAATGCTTTAGCTTGTTGGAATTCTTCTA
ATCCTGAAATCATTGGGAACATTACTGCAAGATTTCCATAAACAGAAGCTCTTAATAAAGCTCTTATTTGAACTC
TAAAGATATCTTTTCTGTCTAAGCATAATCTTATAGCTCTGTATCCCAAGAACGGATCNNTNNTCNTTAA

SEQ ID NO. 374 Bacillus mycoides

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SEQ ID NO. 375 Streptococcus oralis

CNNTTTCCCTTCGCGTGAGCTGCTTTGATAACGTTGTTGATCAGCGTAGGATTGATGGGTTGTATAGGTTGGTAAA
GGTATGAAACTTGCTCGTTCATACGGTCTGCTGCCATTGTGTATTGGATCAAGTCGTTTGTACCAATTGAGAAGA
AGTCAACTTCTTTAGCAAATTGGTCTGCAAGCATTGCTGCTGCAGGAATTTCGATCATGATACCAACTTTGGATAT
TATCCGCAACTGCAACACCTTCAGCAAGAAGGTTTGCTTTTTCTTCGTCAAAGACTGCTTTCGCTGCACGGAATT
CTTTCAAGAGCGCAACCATTGGGAACATGATACGTAATTGACCGTGAACAGACGCACGAAGAAGAGCACGGATTT
GTGTGCGGAACATAGCATCTCCAGTCTCAGAGATAGAGATACGAAGAGCACGGAATCCNAAGAACGGATCNTTTC
TCTTA

SEQ ID NO. 376 Enterococcus hirae

SEQ ID NO. 377 Enterococcus avium

SEQ ID NO. 378 Staphylococcus saprophyticus

TCGTAAGAAGCTTCTATTACTTGTTTTACTAAACGTAATATTGAAGGATTATATGGTTGATACAAGTAAGAAACA
CGTTCTGACATTCTATCAGCAGCCATTGTATATTGAATTAAATCATTCGTTCCTATACTGAAGAAATCATCTCT
TTAGCAAATACATCTGCCAACGCAGCAGTAGAAGGAATTTCTACCATAATACCAAGTTCGATATCATCAGAAACT
TCAATGCCTTCATTTGTTAAGTTATCTTTTTCTTCAAGTAACAATGCTTTAGCATCACGGAACTCTTGGATTGTA
GCTACCATAGGGAACATGATATTCAATTTACCAAAAGCAGATGCACGTAATAATGCACGCAACTGTGGTCTGAAA
ATATCAGGTTGATCTAGGCATAAACGGATAGCACGGTAACCCAAGAACGGATCATTCTCTTA

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SEQ ID NO. 379 Staphylococcus haemolyticus

SEQ ID NO. 380 Enterococcus flavescens

SEQ ID NO. 381 Enterococcus casseliflavus

SEQ ID NO. 382 Enterococcus gallinarum

SEQ ID NO. 383 Enterococcus raffinosus

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SEQ ID NO. 384 Enterococcus villorum

SEQ ID NO. 385 Clostridium difficile

TTTNNGGANGGCNTCTNTCGTANGCATTGTCTATANCAGTCTTTATAAGTCTTAAAACAGCTGGATNAAATTGAT
TGTAAAGNTAACTTATCTTTTGATTCATTCTATCAACTGCACAAGTGTATTGAATTAAATCATTAGTTCCTATAG
AGAAGAAATCTACGTGTTTAGCCAATACATCAGATATCACAGCAGCAGCAGATGGAACTTCTATCATCATACCAATTT
CTACATCTTTAGCATAAGCCACACCTTCAGAATCAAGTTCTGCTAAAACTTCTTTTACAACTTCTTTAGCTTGTA
ACAACTCTTCTAAAGATGAAATCATTGGGAACATGATTCTTAATCTTCCATGAACACTAGCTCTATATAAAGCTC
TCAATTGAGTCTTAAATATATCTTTTCTATCTAGGCAAAGTCTTATTGCTCTGTAACCCAAGAACGG

SEQ ID NO. 386 Streptococcus mitis

SEQ ID NO. 387 Bacillus halodurans

SEQ ID NO. 388 Bacillus weihenstephanensis

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SEQ ID NO. 389 Streptococcus species

CNNANTTNCCTTCGCGTGAGCTGCTTTGATAACGTTGTTAATCAACGAAGGATTGATGGTTGTTATGGTAA
AGGTATGAAACTTGTTCGTTCATACGGTCAGCAGCCATTGTGTATTGGATAAGGTCGTTTGTTCCGATTGAGAAG
AAGTCAACTTCTTTCGCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTGGATA
TCATCTGAAACGGCAACACCTTCAGCTTTAAGGTTTGCTTTTCTTCATCAAAGATTGCTTTAGCAGCACGGAAT
TCTTTAAGAAGAGCAACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATT
TGTGTACGGAACATTGCATTTCCTGTTTCTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGATCCTTT

SEQ ID NO. 390 Streptococcus gordonii

NTGCCTTCGCATGAGCCGCCTTGATAACATTGTTGATCAAGCGAAGGATAGATGGGTTATAAGGTTGATAGAGGT
AAGAGACTTGTTCATTCATCCGGTCAGCTGCCATAGTGTACTGGATCAAGTCGTTGGTACCAATTGAGAAGAGT
CAACTTCCTTGGCAAATTGATCCGCCAACATAGCTGCTGCTGGAATTTCAATCATGATACCCACTTGAATGTTAT
CCGCTACAGCAACACCCTTCAGCTTGCAATTTCGCTTTTTCTTCTTCGTAAACTGCTTTAGCCTTACGGAATTCTG
TTAGAAGGGCTACCATTGGGAACATGATACGTAATTGTCCATGTACAGACGCCACGTAAGAGAGCCCGGATTTGTG
TACGGAACATAGCATTACCAGTTTCAGAGATAGAGATACGCAAAGCACGGAAGCCNAAGAACGGTCNTTTT

SEQ ID NO. 391 Streptococcus canis

CNCGTGAGCTGCTTTGATAACGTTGTTAATCAAACGAAGGATTGATGGGTTGTATGGTTAGGTAAAGGTATGAAAC
TTGTTCGTTCATACGGTCAGCAGCCATTGTGTATTGGATAAGGTCGTTTGTTCCGATTGAGAAGAAGTCAACTTC
TTTCGCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTCGATATCATCTGAAAC
GGCAACACCTTCAGCTTTAAGGTTTGCTTTTTCTTCATCAAAGATTGCTTTAAGCAGCACGGAATTCTTTAAGAAG
AGCAACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATTTGTGTACGGAA
CATTGCATTTCCTGTTTCTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGTCNTTTTTCTCTAA

SEQ ID NO. 392 Bacillus pumilus

CNTACGCTGCTTCATAACAAGCGTAATCAAACGTAAAATCGCTGGATTGTAAGGCTGGTAAAGATAAGACACTCG
TTCGTTCATTCGATCAGCAGCCATTGTGTATTGAATCAAATCATTTTGTTCCAATACTGAAGAAATCAACTTCTTT
TGCGAATTGGTCTGCGATGACAGCGGTTGATGGAATTTCTACCATTATACCGATTTCAATGGAATCGGATACGTC
TGTACCAGCGGCAACCAATGCTTCTTTTTCTTCAAGTAAAATGGCTTTTTGCTTCTCTAAATTCTGATAATGTCGC
GATCATAGGGAACATGATTTTCAAGTTTCCATATGTACTTGCACGAAGTAAGGCGCGTAGTTGTGTTCTGAAAAT
CTCCTGTTCTTCGAGGCCAAAGGCGGATCGCTCTAAAGCCNAAGAACGGATNTTTTTCNTTAA

SEQ ID NO. 393 Bacillus species

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 ${\tt TCATTGGGAACATAATTTTTAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTTGTACGGAACACAT}\\ {\tt CTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCCNTTNTNCTTTAA}$

SEQ ID NO. 394 Lactococcus lactis

GTGAGCTGCTTTGATNCATTGTTAATCAAACGAAGGATTGATGGATTGTAAGGTTGGTAAAGGTAAGAAACTTGT
TCATTCATACGGTCTGCAGCCATTGTATATTTGGATGAGGTCGTTTGTACCAATTGAGAAGAAATCAACTTCCTTA
GCAAATTGGTCTGCAAGCATTGCTGCTGCTGGAATTTCAATCATGATACCTACTTCGATACCATCTGCAACTGGA
ACACCTTCAGCAATCAATTTTGCTTTTTCTTCGTCATAAATCTTCTTAGCTGCACGGAACTCAGTTACGAGAGCA
ACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGAAGCACGCAAGAGTGCACGCAATTGTTACGGAACATT
CCGTCACCAGCTGTTGAAAGGCTGATACGAAGTGCACGCCATCCCANGAACGGTNNTTTTTTTTAA

SEQ ID NO. 395 Bacillus firmus

SEQ ID NO. 396 Haemophilus influenzae

SEQ ID NO. 397 Streptococcus bovis

SEQ ID NO. 398 Enterococcus durans

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ACGCCTTCGCTCACTAATTTTTGTTTTTCTTCTAAAGATTGCTTTCGCTGCACGGAATTCTTTAAGAGTCGCT ACCATTGGGAACATGATGCGTAAGTTTCCATGAACAGATGCACGTAACAATGCGCGCATTTGTGTACGGAACATT TCGTCACCTAATTCAGACAAGCTGATACGTAGCGCACGATAGCCCCAAGAACGGATNNTTTTCCCTTAA

SEQ ID NO. 399 Streptococcus sanguis

SEQ ID NO. 400 Escherichia coli

SEQ ID NO. 401 Serratia liquefasciens

NTGNCTTCTGCATGAGNATGCATCAATAACCTGTTTGATCAGGCCAAGCACTGATGGGGACATCGGGTTATAGAG
ATGAGAAATCAGCTCATTGCCGCGATCTACCGCCAGAGTATACTGGGTTAGATCGTTTGTCCCAATACTAAAGAA
GTCGACTTCTTTCGCCAGGTGATGAGCAATCACTGCCGCGGCCGGTGTTTCCACCATTACGCCCACTTCAATGGT
CTCGTCAAAGGCCTTGGATTCTTCACGCAGCTGCGCCTTCAGCGTCTCGATTTCACCTTTCAGATCGCGGACTTC
TTCCACGGAAATGATCATCGGGAACATGATGCGCAGTTTGCCGAACGCGGAAGCGCGCAGGATGGCGCGCAGTTG
CGCGTGCAGGATTTCTCTGCGGTCCATGGCGATACGAATCGCGCGCCCAAGCACGCNTTNTTTTTTANTTTA

SEQ ID NO. 402 Proteus mirabilis

GTGTGATGCATCACTCTTTTAATCAGATTAAGTACAGCAGGTGACATTGGATTATATAGATGAGATATCAG
CTCATTTCCACGGTCTACAGCCAGAGTATATTGTGTTAGATCGTTAGTCCCAATACTGAAAAAGTCAACTTCTTT
TGCCATATGGCGAGCCATAACAGCCGCTGCTGGCGTTTCAACCATAACACCGACTTCGATAGATTCATCAAAAGG
CTTATTTTCTTCACGAAGCTGGCTTTTCAGTATTTCAAGTTCCGCTTTCAATGCTCGGATCTCTTCAACAGAGAT
AATCATTGGAAACATAATACGTAGTTTACCAAAAGCAGACGCTCTTAAGATAGCACGTAATTGTGGATGAAGGAT
CTCTTTGCGGTCAAGACAAATACGAATTGCACGCCAACCCAAGAACGGAT

SEQ ID NO. 403 Proteus vulgaris

CCTTCTGCATGTGATGCATCAATAACCTGTTTTATCAGGTTAAGTACTGCTGGTGACATTGGATTATACAGATGA GATATCAGCTCATTTCCACGGTCTACAGCCAGAGTATATTGTGTTAGATCGTTAGTCCCAATACTGAAAAAGTCA

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Figure 16 represents marker III (SpyM_0902 & SpyM_0903) sequences amplified from Grampositive bacteria (SEQ ID NOs 404-412).

SEQ ID NO. 404 Streptococcus pyogenes

SEQ ID NO. 405 Streptococcus oralis

SEQ ID NO. 406 Streptococcus faecalis

SEQ ID NO. 407 Streptococcus agalactiae

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SEQ ID NO. 408 Streptococcus pneumoniae

SEQ ID NO. 409 Enterococcus durans

SEQ ID NO. 410 Streptococcus anthracis

SEQ ID NO. 411 Bacillus cereus

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SEQ ID NO. 412 Streptococcus mutans

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Figure 17 represents marker IV (Spy1527, a putative GTP-binding factor plus 160 nt downstream) sequences amplified from Gram-positive bacteria (SEQ ID NOs 413-425).

SEQ ID NO. 413 Listeria monocytogenes

GTTAGAAAAAGGAAGTTCTATTGTAGCATCGCCAAAAATCCATCAAACCTTATTAGATAACTACCTGCCTTAAAG AAAGCGCTCAACATAAAAAAACTTGTTTTCAGAAAATAAAAATCGTGCCAAATCGGCTCAGCTATGCTATAATAG CGATAAATGTTTGGATTTTTAATTTAGGAGGAAACAAGATTGAATTTAAGAAATGATATTCGTAATGTAGCAATT ATTGCCCACGTTGACCATGGTAAAACAACTCTAGTAGACCAATTATTACGCCAGTCAGGCACATTCCGCGACAAT GAAACAGTTGCAGAACGCGCAATGGACAACAATGATTTAGAAAGAGAACGCGGTATTACAATTTTAGCGAAAAAT ACAGCGATTAAGTATGAAGATACACGTGTAAACATCATGGATACACCTGGACACGCCGATTTCGGTGGAGAAGTA GAACGTATCATGAAAATGGTTGATGGTGTTCTTTTAGTAGTGGACGCGTATGAAGGTACGATGCCTCAAACACGT TTTGTACTAAAAAAAGCACTAGAACAAAACCTAACTCCAATCGTAGTAGTAAACAAAATTGACCGTGACTTTGCT CGCCCAGAAGAAGTTGTTGATGAAGTATTAGAATTATTCATCGAACTAGGCGCAAACGACGATCAATTAGAATTC CCAGTTGTTTATGCTTCTGCAATCAACGGAACTTCAAGCTATGATTCCGATCCAGCAGAACAAAAAGAAACAATG AAACCACTTTTAGACACAATTATCGAACATATCCCGGCTCCAGTTGATAATAGCGACGAACCATTACAATTCCAA GTATCATTACTTGATTATAATGACTATGTTGGTCGTATCGGTATTGGCCGCGTATTCCGTGGAACAATGCACGTG GGACAAACAGTTGCTTTAATTAAACTTGATGGCACAGTAAAACAATTCCGTGTAACGAAAATGTTCGGTTTCTTC GGACTAAAACGTGACGAAATTAAAGAAGCAAAAGCTGGTGATTTAGTAGCATTAGCAGGTATGGAAGACATCTTC GTTGGTGAAACAGTAACACCATTTGACCACCAAGAAGCACTTCCGTTATTACGTATTGATGAGCCAACCTTGCAA ATGACTTTCGTAACAATAACAGTCCTTTCGCTGGTCGTGAAGGTAAAACACGTAACAAGCCGTAAAATTGAAGAA CGTTTACTTGCAGAGCTTCAAACGGACGTATCTTTACGCGTAGAGCCAACAGCTTCCCCTGACGCTTGGGTAGTT TCTGGTCGTGGTGAGCTTCATTTATCCATTTTGATCGAAACAATGCGTCGCGAAGGTTATGAATTACAAGTTTCT AAACCAGAAGTAATCATCCGTGAAATTGATGGCGTGAAATGTGAACCAGTAGAAGATGTTCAAATTGATACTCCA GAAGAATTCATGGGTTCCGTTATTGAATCTATCAGCCAACGTAAAGGCGAAATGAAAAACATGATTAACGATGGC AACGGACAAGTTCGTTTACAATTCATGGTTCCAGCTCGTGGCTTAATCGGTTATACAACTGATTTCCTTTCAATG ACTCGTGGTTATGGTATTATCAACCACACA

SEQ ID NO. 414 Listeria innocua

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GACACTATTATTGAACATATTCCAGCTCCAGTTGATAACAGCGACGAGCCATTACAATTCCAAGTTTCTTTACTT
GATTATAATGACTATGTTGGTCGTATTGGTATTGGCCGCGTTTTCCGTGGAACAATGCACGTAGGACAAACAGTT
GCCTTAATTAAACTAGACGGCACAGTAAAACAATTCCGTGTAACGAAAATGTTCGGTTTCTTCGGACTAAAACGT
GACGAAATTAAAAGAAGCAAAAGCGGGTGACTTAGTAGCACTTGCAGGAATGGAAGACATCTTCGTCGGTGAAACA
GTAACACCATTTGACCACCAAGAAGCACTTCCACTTTTACGTATTGATGAGCCAACCTTGCAAATGACTTTTGTA
ACAAATAACAGTCCTTTCGCAGGCCGTGAAGGTAAAACACGTAACAAGCCGTAAAATTGAAGAACGCTTACTTGCA
GAACTTCAAACGGATGTATCTTTACGCGTTGAACCAACAGCTTCTCCAGACGCATGGGTAGTATCTGGTCGTGGT
GAGCTTCACTTGTCTATCTTAATTGAAACGATGCGTCGTGAAGGTTATAAACTAAGTTTCTAAACCAGAAGTA
ATCATCCGTGAAATCGATGGCGTGAAATGTGAACCAGTAGAAGACGTTCAAATTGATACTCCAGAAGAATTCATG
GGTTCAGTTATTGAATCTATCAGCCAACGTAAAGGCGAAATGAAAAACATGATTAACGACGGCAATGGCCAAGTT
CGTTTACAATTCATGGTTCCAGCTCGTGGATTAATCGGTTATACAACTGATTTCCTTTCAATGACACGTGGTTAT
GGTATTATCAACCATACATTCGATAGCTACCAACCAATCCAAAAA

SEQ ID NO. 415 Bacillus cereus

TTACTTTCACAAAAGTAAGAATACAACTATATTTTCATTCTTGCTTTTATTTTAATTGCTATTGTATCCCCTTCG CTCTTATAATAGAGAAGGATTAAAAAGACATTAGGAGTTGGACATGTTGAAAAAACGACAAGATTTACGTAATAT AGCAATTATTGCCCACGTTGACCATGGTAAAACAACACTTGTTGACCAGTTATTACGTCAAGCGGGGACTTTCCG TGCGAACGAACACGTTGAAGAACGCGCAATGGATTCAAATGATCTAGAAAGAGAACGCGGTATTACAATTTTAGC GAAAAATACAGCGATTCACTATGAAGATAAAAGAATTAACATTTTAGATACACCTGGTCACGCTGACTTCGGTGG AGAAGTAGAACGTATCATGAAAATGGTTGATGGTGTTTTACTTGTTGATGCATATGAAGGTTGTATGCCACA AACACGATTTGTTTTAAAGAAAGCTCTTGAGCAAAACTTAACTCCAATCGTAGTTGTAAACAAAATTGACCGTGA CTTCGCTCGTCCAGATGAAGTAGTTGATGAAGTAATCGACTTATTCATTGAGCTTGGTGCAAACGAAGATCAATT AGAGTTCCCAGTTGTATTTGCATCAGCAATGAACGGAACAGCAAGCTTAGATTCAAATCCAGCAAATCAAGAAGA GAATATGAAATCATTATTCGATACAATTATCGAACATATTCCAGCACCAATTGATAACAGCGAAGAGCCACTTCA ATTCCAAGTAGCACTTCTTGATTACAACGACTACGTTGGACGTATTGGAGTTGGTCGCGTATTCCGCGGTACAAT GAAGGTTGGACAACAAGTTGCTTTAATGAAAGTAGACGGAAGCGTGAAGCAATTCCGCGTAACGAAATTATTCGG TTACATGGGATTAAAACGTCAAGAAATTGAAGAAGCAAAAGCAGGGGACTTAGTAGCCGTTTCTGGTATGGAAGA CATTAACGTAGGTGAAACAGTATGTCCAGTTGAACATCAAGATGCGTTACCATTATTACGTATTGATGAGCCAAC ACTACAAATGACGTTCCTTGTAAATAACAGCCCATTTGCAGGTCGTGAAGGTAAATACATTACATCTCGTAAAAT TGAAGAGCGTCTTCGTTCACAATTAGAAACAGATGTAAGTTTACGTGTAGATAATACAGATTCTCCTGATGCGTG GATCGTATCTGGACGTGGGGAACTACATTTATCTATCTTAATTGAAAACATGCGTCGTGAAGGTTATGAATTACA AGTATCTAAGCCAGAAGTAATCATTAAAGAAGTTGATGGCGTAAGATGTGAGCCTGTAGAGCGCGTACAAATCGA TGTACCTGAAGAATACACTGGTTCTATTAT

SEQ ID NO. 416 Bacillus anthracis

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TTGAGCAAAACTTAACTCCAATCGTAGTTGTAAATAAAATTGACCGTGACTTCGCTCGTCCTGATGAAGTAGTTG ATGAAGTAATCGACTTATTCATCGAACTTGGTGCAAACGAAGATCAATTAGAGTTCCCAGTTGTATTTGCATCAG CAATGAACGGAACAGCAAGCTTAGATTCAAACCCAGCAAATCAAGAAGAGAATATGAAATCATTATTTGATACAA TTATTGAACATATTCCTGCACCAATTGATAACAGCGAAGAGCCACTTCAATTCCAAGTAGCACTTCTTGATTACA ACGACTATGTTGGACGTATCGGGGTTGGACGCGTATTCCGCGGTACAATGAAGGTTGGACAACAAGTTGCTTTAA TGAAAGTAGACGGAAGTGTAAAACAATTCCGCGTAACGAAACTATTTGGTTATATGGGATTAAAACGTCAAGAAA TTGAAGAAGCAAAAGCTGGAGACTTAGTAGCTGTTTCTGGTATGGAAGACATTAACGTAGGTGAAACAGTATGTC CAGTTGAACATCAAGATGCGTTACCATTATTACGTATTGATGAGCCAACACTACAAATGACATTCCTTGTAAATA AAACAGATGTAAGTTTACGCGTAGATAATACAGAATCTCCTGATGCGTGGATCGTATCTGGACGTGGGGAACTAC ATTTATCTATCTAATCGAAAACATGCGTCGTGAAGGTTATGAACTACAAGTATCTAAACCAGAAGTAATCATTA AAGAAGTTGATGGCGTAAGATGTGAGCCTGTAGAGCGTGTGCAAATTGATGTACCTGAAGAATACACTGGTTCTA TTATGGAATCTATGGGTGCACGTAAAGGTGAAATGTTAGATATGGTGAATAACGGAAACGGTCAAGTTCGCCTTA $\tt CTTTCATGGTTCCAGCACGTGGTTTAATTGGTTACACAACAGAATTCTTAACATTAACTCGTGGTTACGGTATTT$ TAAACCATACATTCGATTGCTACCAACCAGTACACGCTGGACAAGTTGGTGGACGTCGTCAAGGTGTTCTAGTTT CACTTGAAACAGGAAAAGCATCACAATACGGTATTATGCAAGTTGAAGACCGTGGTGTAATCTTCGTTGAACCAG GTACAGAAGTATATGCTGGTATGA TTGTTG

SEQ ID NO. 417 Staphylococcus aureus

GACTAATAAAAGAGAAGATGTCCGCAATATAGCAATTATTGCTCACGTTGACCATGGTAAAACAACTTTAGTAGA TGAGTTGTTAAAACAATCTGGTATATTCAGAGAAAATGAACATGTCGATGAACGTGCAATGGACTCTAACGATAT CGAAAGAGAGCGTGGAATTACGATTCTAGCCAAAAATACGGCTGTTGATTATAAAGGTACACGTATTAATATTT GGATACACCAGGACATGCAGACTTTGGTGGAGAAGTAGAACGTATTATGAAAATGGTTGATGGGGTTGTCTTAGT AGTAGATGCGTATGAAGGTACAATGCCTCAAACACGTTTTGTACTTAAAAAAGCGCTAGAACAAAACCTGAAACC TGTTGTTGTTGATAAAATTGATAAACCATCAGCACGTCCAGAGGGTGTTGTAGATGAAGTTTTAGATTTATT TATTGAATTAGAAGCAAACGATGAACAATTAGAATTCCCTGTTGTTTATGCTTCAGCAGTAAATGGAACAGCTAG CTTAGATCCTGAAAAACAAGATGATAATTTACAATCATTATATGAAACAATTATTGATTATGTACCAGCTCCAAT TGATAACAGTGATGAGCCATTACAATTCCAAGTAGCATTGTTGGACTACAATGATTATGTTGGACGTATTGGTAT TGGTCGTGTATTCAGAGGTAAAATGCGTGTCGGAGATAATGTATCACTAATTAAATTAGACGGTACAGTGAAAAA CTTCCGTGTAACTAAAATCTTTGGTTACTTTGGATTAAAACGTTTAGAAATTGAAGAAGCACAAGCTGGAGATTT AATTGCTGTTTCAGGTATGGAAGACATTAATGTTGGTGAAACTGTAACACCACATGACCATCAAGAAGCATTGCC AGTTCTACGTATTGATGAGCCTACTCTTGAAATGACATTTAAAGTTAACAATTCTCCATTTGCTGGCCGTGAAGG TGACTTTGTAACAGCACGTCAAATTCAAGAACGTTTAAATCAACAATTAGAAACAGATGTATCTTTGAAAGTTTC TAACACAGATTCTCCAGATACATGGGTAGTTGCTGGTCGCGGTGAATTGCATTTATCAATCCTTATTGAAAATAT GCGTCGTGAAGGTTATGAATTACAAGTTTCAAAACCACAAGTAATTATTAAAGAAATAGATGGTGTAATG

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SEQ ID NO. 418 Staphylococcus epidermidis

AAGAAAGGAATTTATAAAATGACTAATTTAAGAGAAGATGTTCGTAATATAGCGATTATTGCGCATGTCGACCAT GGTAAAACAACATTAGTAGACCAGTTGCTTAAACAATCAGGTATATTTCGTGAAAACGAACATGTCGACGAGCGT GCAATGGACTCTAATGATTTAGAAAGAGAACGTGGTATTACGATTCTTGCTAAGAATACAGCGATAGATTATAAA GGAACGCGTATCAATATATAGACACACCTGGCCACGCCGATTTTGGTGGTGAAGTTGAACGTATCATGAAAATG GTTGACGGTGTCGTACTAGTGGTTGACGCATATGAAGGTACAATGCCTCAAACTCGTTTTGTTCTTAAAAAAGCT TTAGAACAAAACTTAAAACCGGTTGTAGTTGTGAATAAAATTGATAAACCAGCTGCTAGACCTGAGGGAGTTGTA GATGAAGTATTAGACTTATTCATTGAATTGGAAGCGAATGATGAGCAATTAGACTTCCCAGTTGTTTATGCTTCA GCTGTGAATGGAACAGCAAGTTTAGACTCTGAAAAGCAAGACGAAAATATGCAATCCCTATACGAGACGATTATT GACTATGTACCGGCACCAGTAGATAATTCAGATGAACCATTACAATTCCAAATTGCTTTACTAGATTATAATGAT TATGTAGGTCGTATAGGCGTTGGACGTGTTCAGAGGTAAAATGCGTGTAGGTGATAATGTATCACTAATTAAA TTAGATGGTACAGTTAAGAACTTTCGTGTGACGAAAATATTTGGTTACTTTGGTCTTAAACGTGAAGAAATTGAA GAAGCACAAGCAGGAGACTTAATAGCTGTTTCAGGTATGGAAGATATTAACGTTGGTGAAACAGTTACACCACAT GATGTTTCTTTAAAAGTTACACCTACTGATCAACCAGATTCATGGGTTGTTGCTGGTCGTGGTGAACTACACTTG TCTATTCTTATTGAAAACATGAGACGTGAAGGCTTTGAATTACAGGTTTCTAAACCTCAAGTTATTTTAAGAGAA ATCGATGGTGTTAAGTGAACCATTTGAGCGTGTACAATGTGAA

SEQ ID NO. 419 Bacillus subtilis

GAAAAACGTGACGCTTTTAAAGAGGATGTGTGATATAATATGAAAGTTATCTAATTTTTTTAGGAGATGAAAAAG TGAAACTTCGAAATGATCTTCGCAACATCGCGATTATTGCCCACGTTGACCATGGGAAAACGACTCTAGTCGATC AGCTTTTACATCAGGCTGGTACGTTCCGTGCCAACGAACAGGTTGCTGAACGCGCAATGGACTCTAATGATCTTG AACGCGAACGCGCATTACAATATTGGCGAAAAATACTGCGATTAACTATAAAGATACACGTATCAATATTTTGG ACACCCCTGGACATGCAGACTTTGGGGGAGAAGTAGAACGGATTATGAAAATGGTTGACGGCGTAGTGCTTGTCG TTGACGCATATGAAGGCTGTATGCCTCAAACTCGTTTTGTTCTGAAAAAAGCTCTTGAGCAAAACCTGAACCCTG TTGTTGTTGTAAACAAATTGACCGTGACTTTGCTCCTCCAGAGGAAGTTATCGATGAAGTTCTGGATCTGTTCA TTGAGCTTGATGCCAATGAAGAGCAGCTCGAGTTCCCAGTGGTATATGCTTCCGCGATTAATGGAACAGCGAGTC TTGATCCGAAACAGGATGAAAACATGGAAGCTTTATATGAAACCATTATTAAGCATGTTCCGGCACCTGTTG ATAATGCAGAGGAGCCGCTTCAATTCCAAGTTGCCCTTCTTGACTACAACGACTATGTAGGCCGTATCGGAATCG GACGCGTATTCCGCGGCACAATGAAAGTCGGACAGCAGGTTTCTCTTATGAAGCTTGACGGAACGGCAAAGTCAT TCCGTGTTACAAAGATTTTTGGTTTCCAAGGCTTAAAGCGTGTGGAAATTGAAGAAGCAAAAGCGGGAGACCTCG TTGCGGTTTCCGGGATGAAGATATCAACGTTGGTGAAACGGTATGTCCTGTAGACCATCAAGATCCGCTTCCGG TCCTTCGCATTGATGAGCCGACACTTCAAATGACATTTGTCGTGAATAACAGTCCGTTTGCAGGCCGTGAAGGCA AATATGTAACGGCCCGCAAAATCGAAGAGCGTCTTCAATCACAGCTTCAGACGGATGTGAGCTTGCGTGTTGAGC CAACAGCTTCTCCTGATGCTTGGGTTGTTTCAGGACGCGGTGAGCTGCACTTGTCAATTTTAATTGAAAATATGC GTCGTGAGGCCTATGAGCTTCAAGTGTCAAAACCTGAAGTTATTATCAAAGAAATCGACGGCGTACGCTGTGAGC CTGTTGAACGTGTGCAAATTGATGTTCCTGAAGAGCATACTGGCT

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SEQ ID NO. 420 Streptococcus mutans

GGAATGGAAAAGTAAAAGAGAAGAATTAGTTCTTTTTTGAGATAATGACAGGGATTAGTATGAGCTGTTGTCTTT TGTTTTTGCAATACTGGTTGATTGAGGACTTATTTTATAAAATTTGGAGATACCAAGACTGCGACTTTGCTATCT TGGTTTTTCTTTTATATTTTAAAACATTTACATATCTCTCCTGAGTTTTTCCCTAATTTTTATGGTATAATAGAT AAGTTGAAATAAATTAATGTAAAATGTAAGAGGAATTATGACAAATTTTAGAGAAGATATTAGAAATGTTGCTAT CATTGCCCACGTTGACCATGGGAAAACAACCCTTGTTGATGAGCTCTTAAAACAATCGCATACACTTGATGAGCA TAAAAAATTAGAAGAACGTGCGATGGACTCTAATGATCTTGAAAAAGAGCGTGGGATTACTATTCTTGCAAAAA TACTGCTGTTGCCTACAATGGTGTACGTATTAACATTATGGACACCAGGACATGCGGATTTTGGTGGAGAAGT AGAGCGTATCATGAAAATGGTTGATGGGGTTGTTCTTGTTGTTGATGCTTATGAAGGTACCATGCCGCAAACACG TTTTGTTTTGAAAAAGCTTTGGAACAAACCTGGTTCCAATCGTGGTGGTGAATAAGATTGACAAGCCATCAGC ${\tt TCGTCCGCAGAAGTTGTTGAAGTTCTTGAACTTTTCATTGAACTTGGAGCAGATGATGACCAGTTAGAGTT}$ TCCAGTCGTTTACGCTTCGGCGATTAATGGAACTTCTTCATTATCAGATGAACCAGCGGATCAAGAACATACAAT AGTGTCTCTCCTTGATTATAACGACTTTGTTGGACGTATCGGTATTGGGCGAGTCTTCCGTGGTTCTGTTAAAGT CGGGGATCAAGTGACACTTTCTAAACTTGATGGTACAACAAAGAATTTTCGTGTTACAAAACTTTTCGGTTTTCTT $\tt CGGTTTGGAACGTCGTGAGATTAAGGAAGCTAAGGCTGGCGATTTGATTGCTGTTTCAGGTATGGAAGATATCTT$ TGTTGGTGAAACGATTACACCAACTGATGCTGTAGAACCACTTCCTATTCTTCACATTGATGAGCCAACTCTGCA AATGACCTTTTTAGCTAACAATTCCCCTTTTGCAGGCCGTGAAGGTAAATTTGTAACCTCGCGTAAGGTAGAAGA GCGTTTGTTGGCAGAATTGCAAACAGATGTTTCCCTTCGTGTAGAAGCCACTGACTCACCAGATAAATGGACGGT TTCAGGTCGTGGGGAGTTACATCTGTCAATCCTTATTGAAACCATGCGCCGTGAAGGATATGAGCTGCAAGTATC GCGTCCAGAAGTTATTATCAAAGAAATTGATGGCATCAAATGTGAGCCATTTGAACGCGTGCAAATTGACACACC GGAAGAATACCAAGGTGCTGTTATCCAGTCCCTTTCAGAACGTAAAGGTGAAATGCTTGA

SEQ ID NO. 421 Streptococcus pneumoniae

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CAGGCAGAATTGCAAACAGACGTTTCCCTTCGTGTTGACCCAACTGATTCACCAGATAAATGGACTGTTTCAGGA CGTGGAGAATTGCACTTGTCAATCCTTATCGAAACAATGCGTCGTGAGGGCTATGAACT

SEQ ID NO. 422 Streptococcus agalactiae

AATAGGCAGTTAATATGAAAACATTTACACTTGTGTAAATTCTGTTTTTTAAGAAAAATTGTGTTATAATTCATA AGTTAACAGAATTACATTATAAAATAGAGGAAAACATGACAAATTTAAGAACAGATATCCGTAACGTTGCGATCA TTGCCCACGTTGACCACGGTAAAACAACTCTCGTTGATGAATTATTAAAACAATCACATACTCTTGATGAGCGTA AAGAGCTTGAAGAACGTGCAATGGATTCAAATGATATCGAAAAAGAACGTGGTATCACCATTCTTGCAAAAAATA CAGCCGTAGCATACAACGATGTTCGTATCAATATTATGGACACCTGGTCACGCGGACTTTGGTGGTGAAGTTG AGCGTATTATGAAAATGGTTGATGGTGTTTTTAGTCGTTGATGCCTACGAAGGAACAATGCCACAAACACGTT CTGTTGTTTATGCTTCAGCTATCAATGGAACATCTTCAATGTCAGATGATCCTTCAGATCAAGAAAAAACAATGG CACCGATTTTTGATACTATCATTGATCACATTCCAGCCCCAGTTGACAACTCGGAAGAACCACTTCAATTCCAAG TTTCTCTTCTTGATTACAATGATTTTGTAGGACGTATTGGTATTGGACGTGTTTTCCGCGGGGACTGTCAAAGTTG GAGATCAAGTTACTCTTTCAAAACTTGATGGTACAACTAAAAACTTCCGCGTAACAAAACTTTTTGGTTTCTTTG GACTTGAACGTAAAGAAATCCAAGAGGCTAAAGCGGGTGATTTAATCGCTGTTTCTGGTATGGAAGATATCTTCG TTGGTGAGACAGTAACTCCGACAGATGCTATTGAACCACTACCAGTTTTACGTATTGACGAGCCAACACTTCAAA TGACTTTCTTGGTGAATAATTCACCATTTGCAGGTCGCGAAGGTAAATGGATTACGTCACGTAAGGTTGAAGAAC GTCTTTTAGCAGAATTACAAACAGACGTTTCTTTACGTGTTGACCCAACAGATTCGCCAGATAAATGGACGGTTT CAGGGCGTGGAGAATTACATTTATCTATCCTTATTGAAACAATGCGTCGTGAGGGATATGAACTTCAAGTATCAC GTCCAGAAGTTATCATCAAAGAAATTGATGGTGTTCAATGCGAGCCGTTTGAGCGTGTTCAAATTGATACTCCAG CACGTGGATATGGTATCATGAATCATACTTTTGACCAGTATCTACCGGTTGTTCAAGGAGAAATTGGTGGTCGTC ATCGTGGTGCCTTGGTTTCTATTGAAAATGGTAAAGCAACTACATATTCAATTATGCGTATTGAAGAACGTGGGA CTATCTTTGTAAATCCAGGTATAGAAGTTTATGAAGGAATGATTGTTGGTGAGAATTCTCGTGATAATGACCTCG GAGTCAATATTACAACTGCTAAACAAATGACAAATGTCCGTTCAGCAACTAAAGATCAAA

SEQ ID NO. 423 Streptococcus pyogenes

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SEQ ID NO. 424 Enterococcus faecalis

GAAGAATTTGGGTTTAAATACTCTGGTATTACAGGAAAACCATTAACTTTTGCGGGTCGTGAATACTTTATTGCA GCAACTCCTGAAACCTATGATGAAGTATTTACCCGATATTTAAATGAATCGGAATAATCAAAGAAGAGCGTTGCT GAAAGGTAAGGCTCTTCCTCTTTTAAAAGAGAAAAATTTGTAAAAAAATGTCCTTGTTTTCAGAAAAAGCCGAAT GGCTTTTATGGACTTAAGTAACATAAGCGTATATAGATAAGGAGCAATTAAATTGAAATACAGAGATGATATTCG TAACGTGGCAATTATCGCCCACGTTGACCATGGTAAAACAACCTTAGTAGATGAACTTTTAAAACAATCTGACAC TTTAGATGGACACACAATTACAAGAACGTGCAATGGATTCCAATGCACTTGAAAGTGAACGTGGAATTACTAT CTTAGCAAAAAATACAGCCGTAGATTATAACGGTACACGTATCAACATTCTAGATACACCAGGACACGCGGACTT CGGTGGTGAAGTAGAACGTATCATGAAAATGGTAGACGGTGTTGTTTTAGTTGTCGATGCGTATGAAGGAACAAT GCCTCAAACACGTTTCGTATTGAAAAAAGCATTAGAACAAAAAGTAACACCAATCGTGGTTGTTAACAAAATTGA CAAACCTTCTGCTCGTCCTGAACACGTAGTAGATGAAGTTTTAGAGTTATTCATCGAATTAGGTGCAGACGACGA TCAATTAGATTTCCCAGTTGTTTATGCTTCTGCTTTAAACGGAACTTCAAGTGAATCAGATGATCCAGCAGATCA AGAGCCAACAATGGCCCCAATTTTTGATAAAATTATTGAACATGTGCCAGCTCCAGTTGACAATTCAGACGAACC ACTTCAATTCCAAGTCTCATTACTAGACTACAACGATTACGTTGGACGTATTGGGATTGGCCGTGTTTCCGTGG CACAATGAAAGTCGGCGACCAAGTTGCGTTGATGAAAATTAGATGGCAGCGTGAAAAATTTCCGTGTAACGAAAAT TTTAGGTTTCTTTGGCTTACAACGTGTGGAAATTGATGAAGCAAAAGCGGGCGATTTAATTGCCGTTTCTGGAAT GGAAGACATTTTCGTTGGGGAAACAGTTGTAGATGTTCACAATCAAGAAGCATTACCAATTCTACACATTGATGA GCCAACCTTACAAATGACTTTCTTAGTTAACAATTCTCCATTTGCGGGACGTGAAGGAAAATACATCACCGCTCG TAAAATCGAAGAACGTTTAATGGCTGAGTTACAAACAGACGTATCTTTACGTGTTGATCCAATTGGCCCAGATTC TTGGACTGTATCAGGTCGTGGCGAATTGCATTTATCAATTTTAATTGAAAACATGCGTCGTGAAGGCTATGAATT ACAAGTTTCTCGTCCAGAAGTTATTGAACGTGAAATTGATGGAGTTAAATGTGAACCATTTGAACGTGTTCAAAT TGACACACCTGAAGA

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SEO ID NO. 425 Lactococcus lactis

CGAAAAAGCAAGTTAAATATGTTGTAAATAATGGTGTTACATTAGATAATACTAGTGGTGGGCCTAATTTGGCTG CACCTGTGACGGTGGATAGTCAGGTAATTTCGAACGATAAAGGTACGATTATGGGTGTAAGGACCTATACAGCAG ATTTAAGCCAAGCAGAAGTAGTTAAAAAAGTGGGTAATTTGAATGCAATGTCCTTTGGAGAATTTTGGGGTACAA AAGTTTTTGCTGCCAGCCAAAATCAGACAAATTCAGATAAGACTTATTCTGTTACGTTTAAACTGAATATAAATT GGATAGTATCTAATGGCTATGCTTCGCTAACAAAAGTAACAGGTGGCTATGGTTCTTGCATTGACCATGTTTATG TTGCTAATTCTAGTGTTACTACTGCAACGAATGGTCAGATTAAAGGTTCAAGTGGTTATACTCAACAAGTTGATG ACAAATCAGAAGGGAATAGTTTATCGTGGTCAATTACGCGAAACTATAAACCTGTAAAAGTTCCAGCAAGTGGGG CAAATGTAGGAGCTACGTATTTTGCCACACTTAAACGGGGAAATAGTACATGGAAATTCCAAACAACAAATAGAG CTTATTAAGTGGGAGGAAGTGGAATGAATATAAAAGGCATAAAAATTTGGCAAGTATTTCTTGCATTCATCATTT GGATAGGAACCATGTTTCTTCCTGCAACGGTAAATCAGGCTAAATTGAATACGAATTTTGACTATAAAAAAAGTC GAGAAAATTTCTTTTATTTTCTTTTCATCAAGTCCCTTTTTATAGTTTCATTTTGGGATTGGTGTTGCTTATAT CACTTTTTCTCATTTATAGGAAAATAAATTTTAGTGTCTATTTTTCTTTTGCTAGTCTTATTTTTTACATTAGTT TCTTAGTTATAGCTTTTCCGTCTATGATTATTTTTAATCATAGTTTATCTGGGAATACTTTTGGGGCTGAACTTT CTATCTTCTAACCTTTTATGGAGCTGGATATTATTATTGCTGTTCTATTTGGTTTAGTTGCTTTTCTTTTACTCT AAGAACTCCTTAGAAATTTTTCTTTGGGGTTTTCATTTTGGAAGTAAAAAAATCTTTGTTAGGCTTGTAAACGTG TGCATTTACAGCTTTTAGAAAAGTGTGCTATAATGGGTTAGATATACGAAAGTAAGGTATGATAAAATTGACT AAATTACGCGAAGATATTAGAAACGTCGCTGTTATTGCCCACGTTGACCATGGTAAAACTACATTGGTTGACGAA CTCTTAAAACAATCTCAAACGTTGGATGCTCGTAAAGAATTAGCTGAACGTGCGATGGACTCAAATGCACTTGAG CAAGAACGTGGGATTACTATCCTTGCCAAAAATACAGCAGTTGAATATAACGGAACTCGTATCAACATCTTGGAC ACACCAGGTCACGCGGACTTCGGTGGAGAAGTTGAACGTATTATGAAAATGGTTGATGGGGTTGTCCTCGTTGTC GATGCTTATGAAGGAACAATGCCTCAAACACGTTTTGTTTTGAAA

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Figure 18 represents sequences amplified with molecular marker VI (pgi) from various Gramnegative bacteria (SEQ ID NOs 426-430).

SEQ ID NO. 426 Citrobacter freundii

SEQ ID NO. 427 Klebsiella pneumoniae

ATCTGGTACAACAACTTCTTCGGTGCGGAAACCGAAGCGATTCTGCCGTACGACCAGTACATGCACCGCTTTGCC
GCTTACTTCCAGCAGGGCAACATGGAGTCCAACGGTAAGTATGTTGACCGTAACGGCCACGCGGTAGACTACCAG
ACTGGCCCAATCATCTGGGGTGAGCCGGGCACCAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGCACC
AAAATGGTACCGTGCGATTTCATCGCTCCGGCTATCACCCACAACCCGCTGTCTGACCACCATCAGAAACTGCTG
TCTAACTTCTTCGCCCAGACCGAGGCCCTGGCCTTTGGTAAATCCCGCGAAGTGGTTGAGCAGGAATATCGCGAT
CAGGGTAAAGACCCGGCGACCCTGGAGCACGTGGTGCCGTTCAAAGTGTTCGAAGGTAACCGCCCGACTAACTCC
ATCCTGCTGCGCGAGATTACCCCGTTCAGCCTCGGGGGCGCTGATTGCCCTGTACGAGCACAAAATCTTCACCCAG
GGCGCGATCCTCAACATCTTCACCTTTGACCAGTGGGGCGTTGAGCTGGCCAAACAGCTGGCTAACCGCCTCATA
CCGGAGCTGAAAGACGGCAGCGAAGTTAGCAGCCACGACAGCTCTACTAACGGCCTGATTAACCGCTATA

SEQ ID NO. 428 Klebsiella oxytoca

ATCTGGTACAACACTTCTTCGGCGCTGAAACCGAAGCGATTCTGCCGTACGACCAGTATATGCACCGCTTTGCC
GCCTACTTCCAGCAGGGCAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAG
ACGGGCCCGATCATCTGGGGCGAGCCGGGCACCAACGGTCAGCACGCGTTCTATCAGCTGATTCACCAGGGGACC
AAAATGGTGCCGTGCGATTTTATCGCTCCGGCGATTACGCATAACCCGCTGTCTGACCATCATCCGAAGCTGCTG
TCTAACTTCTTTGCGCAGACCGAAGCGCTGGCGTTTGGTAAATCCCGCGAAGTGGTTGAACAGGAATATCGCGAT
CAGGGTAAAGATCCCGCGACGCTGGAACACGTGGTGCCGTTCAAAGTGTTTGAAGGCAACCGCCCGACTAACTCC
ATCCTGCTGCGTGAAATCACGCCGTTCAGTCTGGGCGCGCTGATTGCCCTGTATGAACATAAGATTTTCACCCAG
GGCGTGATTATGAACATCTTCACCTTCGACCAGTGGGGCGTTGAGCTGGGCAAACAGCTGGCGAACCGCATCCTG
CCGGAGCTGAAGGATGGTTCTGAAGTCAGCAGCCACGACAGCTCCACTAACGGCCTGATTAACCGCTATA

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SEO ID NO. 429 Escherichia coli

SEQ ID NO. 430 Serratia marcescens

AAGCACTTTGCCGAAACGCCGGCGGAGAAAAACCTGCCGGTGTTGCTGGCGCTGATCGGTATTTGGTACAACAAC
TTCTTTGGCGCCGAAACCGAAGCCATTCTGCCGTACGATCAGTACATGCACCGTTTTTGCCGCTTACTTCCAGCAG
GGCAAGATGGAATCCAACGGCAAGTACGTCGATCGCAACGGCAACCCGGTGGATTACCAGACCGGTCCCGTCATT
TGGGGCGAGCCGGGCACCAACGGCCAGCATGCGTTCTATCAGTTGATCCACCAGGGCACCAAGCTGGTGCCGTGC
GATTTCATCGCGCCGGCCATCAGCCATAACCCGCTGGGCGATCATCACGCCAAACTGCTGTCCAACTTCTTCGCT
CAGACCGAAGCGCTGGCGTTCGGCAAGTCGCTGGAAGTGGTGGAAGCCGAGTTCGCGGCGCAGGGCAAAACTCCT
GAGCAGGTCAAGCACGTGGCGCCGTTCAAGGTGTTTGAAGGCAACCGGCCG

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Figure 19 represents sequences amplified with molecular marker V (carB) from various Gram-negative bacteria (SEQ ID NOs 431-442).

SEQ ID NO. 431 Neisseria gonorrhoeae

SEQ ID NO. 432 Serratia marcescens

SEQ ID NO. 433 Citrobacter freundii

TCGCCCTTCGACTATTATGACTGACCCGGAAATGGCCGATGCCACCTACATCGAGCCGATTCACTGGGAAGTGGT ACGCAAAATCATTGAGAAAGAGCGCCCGGATGCGGTGCTGCCAACCATGGGCGGTCAGACGGCGCTGAACTGTGC

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SEQ ID NO. 434 Enterobacter aerogenes

SEQ ID NO. 435 Enterobacter cloacae

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ACCGTTGCGCCAGCGCAAACGCTGACCGACAAAGAGTACCAAATCATGCGTAACGCATCGATGGCGGTACTGCGT
GAAATCGGCGTCGAAACCGGTGGTTCTAACGTGCAGTTCTCGGTGAACCCGAAAACCGGCCGTCTGATTGTTATC
GAAATGAACCCGCGCGTGTCCCGCTCCTCCGCGCTGCTTCTAAAGCGACCGGCTTCCCGATTGCGAAGGTGGCG
GCGAAACTGGCGGTCGGTTACACCCTTGACGAGCTGATGAACGATATCACCGGGGGCCGCACGCCTGCGTCCTTC
GAACCGTCTATCGACTACGTTGTGACCAAAATTCCACGCTTCAACTTCGAGAAATTCGCTGGCGCAACGACCGT
CTGACCACCCAGATGAAATCAGTCGGCGAAGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCC
GAGCTCGGTACCAAGCTTGATGCATAGNCTTGAGTATTNCTAACGCGTCACCTAAATNGTCTGGCGAA

SEQ ID NO. 436 Morganella morganii

SEQ ID NO. 437 Escherichia coli

CACGACGCCGCCGTTGTTCGACCACTTTATCGAGTTAATTGAGCAGTACAAAACCGCTAAGTAATCAGGA
GTAAAAGAGCCATGCCAAAACGTACAGATATAAAAAGTATCCTGATTCTGGGTGCGGGCCCGATTGTTATCGGTC
AGGCGTGTGAGTTTGACTACTCTGGCGCGCAAGCGTGTAAAGCCCTGCGTGAAGAGGGTTACCGCGTCATTCTGG
TGAACTCCAACCCGGCGACCATCATGACCGACCCGGAAATGGCTGATGCAACCTACATCGAGCCGATTCACTGGG
AAGTTGTACGCAAGATTATTGAAAAAGAGCGCCCGGACGCGGTGCTGCCAACGATGGGCGGTCAGACGGCGCTGA
ACTGCGCGCTGGAGCTGGAACGTCAGGGCGTGTTGGAAGAGTTCGGTGTCACCATGATTGGTGCCACTGCCGATG
CGATTGATAAAGCAGAAGACCGCCGTCGTTTCGACGTAGCGATGAAAAATTTGGTCTGGAAACCGCCGGTTCCG
GTATCGCACACACGATGGAAGAAGCGCTGGCGGTTGCCGCTGACGTGGGCTTCCCGTGCATTATTCGCCCATCCT
TTACCATGGGCGGTAGCGGCGGCGGTATCGCTTATAAACCGTGAAGAATTTGAAGAAATTTGCGCCCGCGGTCTGG
ATCTCTCTCCGACCAAAGAGTTGCTGATTGATGAGTCGCTGAAAAACTTCGATGGGCATCCACACCGGTGACT
CCATCACTGTCGCGCCAGCCCAAACGCTGACCGAAAAAACTTCGATGCGATAACGCCTCGATGGCGTGC
TGCGTGAAATCGGCGTTGAAACCGGTGGTTCCAACGTTCAGTTTGCGGTGAAACCCCGAAAAACGGTCGTCTGATTG
TTATCGAAATGAACCCACGCGTTTCCAACGTTCCACCGTTGAAGACCCGAAAAACGGTCGTCTGATTG

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SEQ ID NO. 438 Proteus mirabilis

SEQ ID NO. 439 Proteus vulgaris

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SEQ ID NO. 440 Neisseria meningitidis

CCAAACGTACCGACCTAAAATCCATCCTTATCATCGGCGCCGGCCCTATCGTTATCGGTCAGGCCTGCGAATTTG ACTATTCGGGCGCACAGGCCTGCAAGGCTTTGCGTGAAGAAGGCTATAAAGTCATTTTGGTGAATTCCAACCCCG CCACGATTATGACCGACCTGAAATGGCGGATGTTACCTACATCGAGCCGATTATGTGGCAGACGGTGGAGAAGA TTATCGCCAAGGAGCGGCCTGATGCGATTCTGCCCACGATGGGCGGTCAGACCGCGCTGAACTGTGCGCTGGATT TGGCACGCAACGCCTGCTGGCAAAATACAATGTCGAGCTGATTGGCGCGACGGAAGACGCGATCGACAAGGCGG AAGACCGCGGCCGCTTTAAAGAAGCGATGGAAAAAATCGGTTTGTCTTGCCCGAAATCTTTTGTCTGCCACACGA TGAACGAAGCTTTGGCGGCGCAGGAGCAGGTCGGCTTCCCGACGCTGATTCGTCCTTCTTTCACGATGGGCGGTT CGGGCGGCGGCATTGCCTACAATAAAGACGAGTTTTTGGCGATTTGCGAACGCGGTTTCGATGCGTCGCCCACGCACGAGCTGCTGATTGAGCAGTCCGTCCTCGGCTGGAAAGAGTACGAGATGGAGGTGGTGCGCGATAAGAACGATA ACTGCATCATCTTTGCTCGATTGAAAACTTCGACCCGATGGGCGTGCATACGGCGACTCGATTACGGTTGCGC CGGCGCAAACATTGACAGACAAAGAATACCAAATCATGCGTAATGCTTCGTTGGCAGTATTGCGCGAAATCGGCG TGGACACGGGTGGCTCAAACGTGCAGTTTGCGGTGAACCCTGAAAACGGCGAGATGATTGTGATTGAGATGAACC $\tt CGCGCGTGAGCCGTTCATCCGCGCTGGCTTCCAAAGCGACGGGCTTCCCGATTGCGAAGGTGGCGGCGAAACTGG$ TTGATTATGTGGTAACCAAAATCCCGCGTTTCGCGTTTGAAAAATTCCCCGCCGCAGACGACCGCCTGACTACGC AGATGAAATCGGTGGGCGAAGTGATGGCGATGGGACGCACGATTCAGGAAAGTTTTCCAAAAAAGCCCTGCGCGGCT TGGAAACAGGCTTGTGCGGCTTCAATCCGAGAAGCTCCGACAAAGCGGAAATCCGCCGCG

SEQ ID NO. 441 Klebsiella oxytoca

SEQ ID NO. 442 Legionella pneumophila

TTCGCCCTTCGACTATTATGACTGATCCTGAGCTTGCTGATGCCACCTATATAGAGCCTGTTCAATGGAAAGAAG
TGGCTCGTATTATCGAAATAGAGAGGCCAGATGCTCTTTTACCGACGATGGGAGGACAAACAGCCTTAAACAGCG
CCTTGGACTTGGTAAGAGAAGGGGTATTAGCCAAGTACTCTGTTGAAATGATAGGAGCGACGCGTGAAGCCATAG

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ACAGGGCGGAAGATAGAGAAAAATTTCGCCAGCTGATGATTAAAATCGGATTGGATATGCCAAGGTCGGCGATTG
CTCATAGCCTGGAAGAAGCAATTCAAGTACAAGCCCGTTTAGGCTTTCCTGCCATCATCAGGCCTTCATTTACCA
TGGGTGGTAGTGGAGGCGGTATTGCCTATAATCGTGAAGAATTTTGAAGAAATTTTGCATTAGAGGATTGGAGTTGT
CGCCAACTCACGAGCTTTTGATTGATGAATCGGTTCTGGGTTGGAAAAAATATGAAATGGAAGTCGTCAGGGATA
AAAATGATAATTGCATTATTGTTTGTACTATAGAGAATTTTGACCCTATGGGAGTGCATACTGGAGATTCCATTA
CCGTTGCTCCGGCACAAACATTAACTGATAAAGAATACCAACGGATGCGGGATGCGGCGATTAAAGTTCTAAGGG
CAGTTGGTGTGGATACGGGAGGTTCCAACGTTCGGTTTGCTATTAATCCTGAAGACGGGCGCATGCTGGTTGTGG
AAATGAACCCGCGTGTATCTCGAAGCTCGGCTTTGGCGTCAAAAGCAACCGGTTTTCCTATTGCTAAGGTCGCAG
CTAAATTGGCTGTGGGCTATACCTTGGATGAATTGAAAAACGAAATCACCGGAGGTAAAACACCTGCGTCCTTTG
AGCCCAGCATTGATTACGTCGTTACCAAAGTTCCACGGTTTTAATTTTGATAAATTTCCACAAACTCCAGATACTC
TTACCACACAGATGAAATCAGTCGGCGAAGTAAGGGCGAATTCCAGCACACTGGCGCCGTTACTAGTGGATCCG
AGCTCGGTACCAAGCTTGATGCATAGNCTTGAGTATTNCTAACGCGTCACCTAAATAGCTGGCGAAA

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Figure 20 represents sequences amplified with molecular marker VII ((EG10839 & EG11396 or sfrB & yigC) in Gram-negative bacteria (SEQ ID NOs 443-451).

SEQ ID NO. 443 Pseudomonas aeruginosa

tecaccagcagegeegegeagatatggeagttgeegttgeggeagetetgeggaeagtegtageeaageegeegg $\verb|cgatcccgaggctcgatcgatcgccgtgtcaccgcttcgtccttgacgatggcgcccccatt|\\$ egeggetggtetegeeeggeeacttgtgggtggeateaageeeeatettegageegaggeeggaaaeeggegagg cgaagtcgaggtagtcgatgggcgtgttgtcgatcatcaccgtgtcgcgcttggggtccatccgcgtggtgatgg occagatcacatcgttccagtcgcgcgcatcgatgtcatcgtcggtgacgatgacgaacttggtgtacatgaact $\tt gccgcaggaacgaccagaccccgagcatcacgcgcttggcgtgccctgggtactgcttcttcatggtcaccaccg$ $\verb|ccatccggtaggaaccaaccttccggcggcaggtagaaatcgacgatttccgggaactgcttctgcaggatcggca|\\$ cgaacacttcgttcagcgccaccccgaggatcgccggctcgtccggcggacgcccggtgtaggtgctgtggtaga $\verb|teggtttctgccggcggtgacgcgctcgacggtgaacaccgggaagcgatcgacctcgttgtagtagccggtgt|$ $\tt gategccataggggccttegteggccatctegeeggggtggateaccccttegaggacgateteggeeggeeggctggccq$ $\tt gcacctgcaagtcgctcccgcgacacttgaccagctcggtacgatgcccgcgcaacaggccggcgaaagcgtatt$ $\verb|cggaaagggtgtccggcaccggcgtcaccgaggatggtcgccggatcggcgcccagcgccacggctaccg|$ gatagggetggeeeggatgettetggeaceaetegeggtagteeagtgegeegeegegatggetgageeagegea $\verb|tgatcaccttgttgcggccgatcacctgctggcggtagatgcccaggttctgccgttccttgttcggcccgcggg|$ taacggtcaggccccaggtgatcagcggcccgacatcgcccggccagcaggtctggaccggccagccgaggt cgacgtcctcgccctcctcgaccacttcctggcagggggcgtccttgagcaccttcggcgccatggacaggacct ${ t tcctgtacatcggcagcttggcccaggcgtccttgaggcccttcggcggctcgggctccttgagttgcgccagca}$ gettgeegatetegegeagtgegeegaegteeteggegeeeatgeeeagegeeaegegeteeggegtaeegaaea ggttgccgagcaccggcatgtcgaagccggtcggcttttcgaacagcaatgccgggcccttggcgcgcaacqtqc $\tt ggtcgcacacctcggtcatctcgagcacgggggaaatcggcacctggatgcgcttcaacgcaccgcgctgctcca$ $\tt gctgggcgatgaaatcgcggagatccttgaacgtcattggcctaaccattcactgcaagaccccacatcctacct$ $\verb|tctgtagcatcggctcgaacaaaggcccgagttcatgggccccctgggtcgaaaggtggttgttatccatgtaca| \\$

SEQ ID NO. 444 Pseudomonas syringae

ccgagcagacatggcagttaccgttgcgacagctttgcgggcattcatggcccagccgctgtgcagcatccagaa tccgctcgcccggcagggtttcgagtaccgcacccgagggctgcaaggttacacgcatcagtctattcccaactg agtccagatctcgtccacccggcgcgtggtggcttcgtccttgacgatcgccctgccccattcgcgggtggtttc ccctggccatttgttagtggcatccaggcccatttttgatcccaatccagacaccggagaggcaaaatcgaggta atcgatggcgtgttgtcgatcatgaccgtgtcgcgcttggggtccatgcgggtggtgatggcccagatcacgtc attccagtcaccgccatttgatgtcgtcatcggtgacgatcacaaatttggtgtacataaactggcgcaggaacga ccagacgcccagcatcacgcgcttggcatggccggggtactgtttcttgatagtcaccaccgccatgcggtaaga gcacccctcgggcggcaggtagaaatcgacgatttccggaaactgcttctgcagaatcgcacagaaccttcgtt

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cagcgccacacccaggatagccggctcgtccggtggacgcccggtgtaggtgctgtggtagatcggcttgatgcg $\verb|gtgggtgatgcgctcgacggtgagcaccggaaagctgtcgacttcgttgtaataaccggtgtgatcgccgtaggg|$ $\tt gccttcgttggccatctcgcccggatgaatcacgccctcaagcacgatttcggcactggcacttgcaggtt$ gctgccacggcacttgatcagctcggtgcgcgagccacgcagtagcccggcgaaggcgtattcggacaggctgtc $\verb|gggcaccggcgtcacggcaccgagaatggtcgccgggtccgcccagtgcgacggccaccggataaggctcgcc|$ ${\tt aggatgcttgacgcaccagtcgcggaagtcaagcgcgccaccgcgatggctgagccagcgcatgatgatcttgtt}$ geggeegatgaeetgetggegataaataeegaggttetgeegeteettgttegggeetttggteaeggteaggee ccaggtgatcagcggcgcgacatcgcccggccagcaggtctgcaccggcaacatgccgagatcgacgtcatcacc $\verb|ctcgatgacgatctccttgacgaccttgggcgccatggcgatgactttgcggaagatggc| \\$ $\tt gcgcagctcggtgacggcttccgcgcccatgcccatggccacgcgctccggcgtgccgaacaggttgcccagcac$ cggaatatcaaagccaaccgggttttcaaaccagcagggccgggcctttggcgcgcaaggtacggtcacagatttc agtcatttccagcacaggcgagatcggcatctgaatgcgtttcaactctccgcgctgctccaactgctgcacgaa atcccttagatctttgaatttcattaacccggccatttatccaaatagacgcacatcgtacctgctcccgccctc tgttacttgcgtttcatggacaggaagaactcgtcgttggtcttggtctgcttgagcttgtcgatgaggaactcg

SEQ ID NO. 445 Bordetella parapertussis

 $\verb|cgcccgcggcattgctacagtcccagcgtgtcccacatggcatccacccggcgcttgaccgcctcgtccatgtgt|\\$ $\verb|atgggcgtgcccc| attcgcggctggtttcgcccggccacttgttggtggcgtccagccccatcttgccgcccagg|$ $\verb|ccggacaccggcgaggcgaa| tcgaggtaatcgatcggcgtgttctcgaccagcaccgtgtcgcgcaccggggtcc| \\$ $\verb|atgcgcgtggtcatggcccagaccacttcggtccagtcgcggggtcgatgtcttcgtcgaccaccacgatgaac|$ ttggtgtacatgaactgccgcagcacgctccacaggccgaacatcacgcgcttggcgtggccggcgtactgcttg cggatcgacaccaccgccaggcggtagctgcagccttccggggggcaggtagaaatcgacgatttcgggcagctgg taggtggagtggtagatggggttgcgccgcatggtgatgcggtccaccgtgaacaccgggaaccagtcctgctcg gaggccggcaccgacaggtcgctgcccagcgccttgacgacctcggtgcgcgagccgcgcagcagcccggcgaac tggtattcggacagcgtgtccggcaccggcgtgaccgcgtccaggatggtggccgggtcggcacccagcgccacg gcgatgggaaacgacttgcccgggtgggcctgggcgtggtcgcggaagtccagcgcgccgccgcggtgcgacagc cagcgcatgatcagcttgttcggccccagcggctgctggcggtagatacccaggttctgccgccgggcgttcggc ccgcgcgtgatcaccaggccccaggcgagcagggcgccacatcgcccggccagcaggtctggatgggcaggcgg cccaggtcgacgtcggcgccttcccagacgatttcctggcaggcggcgctgcgcacggtcttggggctcatgtcc cacagggcggctttcagcatggacaccttggccagcgcgtcgcgcaggcccttgggcgcttcgggcagg gaggccagcagttcgccggtttcgcgcagggcgccgacgtcgtcggcccccatgccccaggcgacccgccgcggc gggccgccggcgcgcagcacccggtcggcaatctcggtcatttccagccgcgtcgagaccggcgcggtgatgcgt

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ttgagttcgccctggcgttcaagctgggcaagaaaatctcggaggtcgcgatacttcaaggcagatcccggcaaa atagttacattcttgaggcaaaacagaggttaacatctgcctcctctcattccacgcaggaggtcccatgcccga tgcgtcagtggccggcctgttccgacagctggcccaaggagtgcaccaccatctcgccgaat

SEQ ID NO. 446 Neisseria meningitidis

 ${\tt acagaaaatcctcgaagacaccctgctggaacaatggcagtggctcaaacctaaagaaccgtaaacatcctgcgt}$ acacaaatgccgtctgaaacgcccccacgcttcagacggcagaccgtaaaacctacaaccccaattcctcccaaa acttgttggtcgcatccaaacccattttgccgccaagtccgctgacggggctggcgaagtcgaggtagtcgatgg $\tt gcgtgttttccatcaaaacggtatcgcgcacggggtccatgcgcgtggttaccgcccagatgacttctttccagt$ $\verb|cgcgcacatccaccatcatccaccacaatgatgaatttggtgtacataaactggcgcaggaacgaccagcagc|\\$ $\verb|ccatcatcacgcgcttggcgtgtccggcgtactgtttttcatgctcaccaccgccatgcggtaggagcagcctt|$ cgggcggcaggtaaaaatcggtgatttcggggaactgcttttgcaaaagcggtacgaacacttcgttcaacgcca tgcgttcgaccgtaaacacggggaaatggtcctgctcgttgtaatagcccgtgtggtcgccgtatggaccttcca tacatttcaccagttccgtccgcgaaccgcgcagcagtccggcaaactggtattcgctcaaggtatcgggaacgg gcgttaccgcgcccaaaatggtggcagggtcgcagccgagcacgacggcgacgggatacggcgtatcgggattga ttaattgttggcggtaaatgccgagattttggcgtttttttgtgcggcccgcgcgtgacggtcaagccccacgtta ccagcggcgcaacgtcttccggccagcaatgctgaatcggaagttgatacaaatcaacgtcttcgccttcccata cgatttcctgacacggcgcatttttcaccacgttcggcgccatgctccaaatgtctttcaagagcggcagtttgg $\tt aaaacgcgtctttaatgcctttgggcggttcgggttctttcaaatacgccagcgtctgcccgatttcgcgcagct$ $\verb|tggacacgctgtccgcgcccatgcccatcgccacacgttcgggcgtgccgaacaggtttgccaacacgggataat|$ catagegegtacegtegggettaactgggtgtteaaacaacaaegeeggeeetteggegegeageaegeggtegg cgatttcggtcatttccaaatgcggggaaacggggtgcgcgatgcgtttgagtttgccctgctgctcgagcatgg $\verb|cgatgaagtcgcgcaggtctttgtatttcatattcatcctttttgtccttttatcctgagcaatccgattcggat|\\$ accgcccctatccttgcctgcgcttcggcatattctatgccgtgataaaagtcgcgtaccagcggatgttcgctg ccttgatggagttgcaacaaaggacgttgaccatcgggttgggtaacgacattgcaatgcaaaccgaaggtgtcg gattcgtaagggggcagccggttgcagatcatgccgaaataaacggcgttttcagggttg

SEQ ID NO. 447 Shigella flexneri

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gaactgttttttgcagaatcggtacaaacacttcgttcaacgccacgcccagtaccgcgggctcatctggcggacg $\verb|cccggtataggtggaatggtaaatcgcatcttcacgctgggtaatatgcgtcacggtaaacaccgggaaattatc| \\$ $\tt gacttcattatagtaacctgtgtggtcaccatacggcccttccggcgccatctcaccaggatcgatatacccttc$ $\verb|caggacg| a tttcggcactggcacttcgaggtcattggaaatacactttactacttcggttttggtgccgcg| \\$ $\tt tagca at ccgg caa acg catactctg a aag cgt at ccgg aacg ggg tg actg caccg ag aat cg tg g cag gat collection of the co$ ggcacccagcgccacagaaaccgggaaacgttcgcccggatgcgccgcacaccactcctgataatccagcgcgcc gccgcgatgcgacagccagcgcataatcagtttgtttttaccaatcagctgctggcgataaatgcccagattctg ccgctctttatgcgggccgcgttacggtcagcccccaggtaatcagcggcggcatcttccggccagcaggt cataatgggaatgcgattgagatcgacgtcatcgccagagacgatttttttgttggcagggcgcaccacgcagtcg ctttgtcggcatgtttaacacctgcttaaactgcggcagtttatcaaacaggtcgcggaaaccttttggcggctc cggctctttcagaaacgccaataatttaccaacttcacgcagcgccgaaacatcttcctgccccatgcccatcgc cacgcgctttggcgtaccgaacaggttgcacagcaccggcattgagtagcctttagggttttcgaacaacagcgc aggcccaccagcacgcagagtgcggtcagcaatttcagtgatttccagatgcggatccaccgggagcgtgatacg ttttagctcaccctgctgttcaagcagcgtcaggaagtcgcgtaaatcgttatatttcatggcgtccattgtagc ctcttaatctgcgcccattatacggcgttcatctttgcaatgctgtaaatttgttaaattagcgtgaactctgac ggtataacgcaaaccggggaatataattaacttagcgtaaagcttttgctatccttgcgccccgattaaacggat

SEQ ID NO. 448 Escherichia coli K12

catgactgctttcgcgtaaaggttgatttcagaagcgccaatatgcagctcgataaaccctttttcatccggcgt ggccgcgtctggcacgatgcggacacgatatacggtatccgtgatagcttctaccgaggtcactttacagcttaa $\verb|ggttgtcatgcgctttctctgtcggatcgataaatagggcaaaaccaaacgcgcatcaggcgcttttaccgttgtt|\\$ aaaaatagccagttcatcccagatggcgtcaatatgcgcgacaacatctggatctttttttgatgggacgtcccca $\verb|ttcacgctgggtttcccccggccatttattcgtggcatccagccccattttttgaacccagcccggagacaggcga||$ ggcaaaatccagataatcaataggcgtattttctaccagaacagtatcccgcgccgggtccatacgggtggtaat $\tt cgcccaaatcacatcgttccagtcgcgttaacgtcatcatcgcaaacgatcacaaatttagtgtacataaa$ $\verb|ctggcgtaagaacgaccatcatgacgcgcttcgcgtgtccggcgtactgttttttgattgtcactac||$ cgccaggcgataagagcagccttccggcggcaggtaaaaatcgacaatttccggggaactgtttttgcagaatcgg cacaaacacttcgttcagtgcgacacccagcaccgcgggctcatctggcggacgcccggtataggtggaatggta aatcgcatcttcacgctgggtaatatgcgtcacggtaaataccgggaaactatcgacttcattatagtaaccggt $\tt gtggtcgccatacggcccttccggcgcagtttcgccttgttcgatatacccttccagcacaatctccgcactggc$ $\tt gggcacttcaagatcattggagatacacttcaccacttcggtcttggtgccacgtagcaatccggcaaacgcata$ ctctgaaagcgtatccggaacgggagtgactgcaccgagaatcgtggcgggatcggcacccagcgccacagaaac cataatcagtttgtttttaccaatcagctgctggcgataaatgcccagattctgccgctctttatgtgggccgcg cgtcactgtcagcccccaggtaatcagcggcgcggcatcttccggccagcaggtcataatgggaatgcgattgag atcgacgtcatcgccagagacgattttttgttggcagggcgcaccacgcagccgctttgtcggcatgttcaatac ttgcttaaactgcggcagtttatcaaacaggtcgcggaaaccttttggcggctccggctctttcagaaacgccaa taatttaccaacttcacgcagcgccgaaacatcttcctgccccatgcccatcgccacgcgctttggcgtaccgaa caggttgcacagcaccggcattgagtagcctttagggttttcgaacaacagcgcaggcccaccggcacgcaaagt

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gcggtcagcaatttcagtgatttccagatgcggatccaccgggagcgtgatacgttttagctcaccctgctgttc aagcagcgtcaagaagtcgcgtaaatcgttatatttcatggcgtccattgtagcctcttaatctgcgcc cattat

SEQ ID NO. 449 Escherichia coli O157:H7

agaagcgccaatatgcagctcgataaaccctttttcatccggcgtcgaggccattgagaacggacgtttgtcgcg ctcatccatcactaccatcaaatactgaccagcacgaaaaagaaaaggccgcgtctggcacgatgcggacacgata tacggtatccgtgatagcttctaccgaggtcactttacagcttaaggttgtcatgcgctttctctgtcggatcga taaatagggcaaaacaaacgcgcatcaggcgcttttaccgttgttaaaaatagccagttcatcccagatggcgtc aatatgtgcgacaacatctggatcttttttgatgggacgtccccattcacgctgggtttcccccggccatttatt $\verb|cgtggcatccagccccatttttgaacccagcccggagacaggcgaggcaaaatccagataatcaataggcgtatt|\\$ ttctaccagaacagtatcccgcgctgggtccatacgggtggtaatcgcccaaatcacatcgttccagtcgcgtgc $\tt gttaacgtcatcatcgcaaacgatcacaaatttagtgtacataaactggcgtaagaacgaccagacgcccatcat$ gacgcgcttcgcgtgtccggcgtactgttttttgattgtcactaccgccaggcgataagagcagccttccggcgg $\verb|caggtaaaaatcgacaatttccgggaactgcttttgcagaatgggaacaaatacttcgttcaacgccactcccag| \\$ taccgcgggttcatctggcggacgcccggtataggtggaatggtaaatcgcatcttcacgctgggtaatatgcgt $\verb|cacggtaaa| taccgggaaactatcgacttcgttatagtaaccagtgtggtcaccatacggtccttctggcgccat| \\$ $\verb|ttcgccttgttcgatatacccttccagcacaatctccgcactggcgggcacttcgagatcattggaaatacactt|$ tgcaccgagaatggttgccggatcagcgcccaacgccacagagatcgggaaacgttcacctggatgcgccgcaca $\verb|ccactcctgata| at \verb|ccagcgcgccgccgccgcgatgcgacagccaacgcata| at \verb|cagcttgtttttaccaatcagttg| academic accast consists and consists and$ $\verb|ctggcgataa| at \verb|gcccagattctgtcgctctttatgagggccacgtgtaa| cggttagcccccatgtaatcagcgg|$ $\verb|cgcggcatcttccggccaacaggtcataatgggaatacggttgagatcgacgtcatcgccagagacgattttttg|\\$ $\verb|ttggcagggtgcaccgcgcagttcgctttgtcggcatgtttaacacctgcttaaactgcggcagcttatcaaacag|$ $\verb|atcgcgaaaacctttttggcggctctggttctttcagaaatgctaataatttaccgacttcacgcagtgctgaaac||$ $\verb|atcttcctggcccatacccatcgctacgcgctttggcgtaccgaacaagttgcacagcaccggcattgagtaccc| \\$ $\verb|tttagggttttcaaacaacagcgcaggcccaccagcagcgtgcggtcagcaatttcagtgatttccagatg|\\$ $\verb|cgggtccaccgggagcgtgatacgttttagctcaccctgctgttcaagcaacgtcaagaagtcgcgtaaatcgtt|\\$ $a \verb|tatttcatggcgtccattgtagcctcttaatctgcgcccattatacggcgttcatctttgcgatgctgtaaatt|$

SEQ ID NO. 450 Bordetella bronchiseptica

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SEQ ID NO. 451 Bordetella pertussis

tgtatgggcgtgccccattcgcggctggtttcgcccggccacttgttggtggcgtccagcccatcttgccgccc aggccggacaccggcgaggcgaaatccaggtaatcgataggcgcgttctcgaccagcaccgtgtcgcgcacgggg ${\tt tccatgcgcgtggtcatggcccagaccacttcggtccagtcgcggggtcgatgtcttcgtcgaccaccacgatg}$ aacttggtgtacatgaactgccgcagcacgctccacaggccgaacatcacgcgcttggcgtggccggcgtactgc ttgcggatcgacaccaccgccaggcggtagctgcagccttccgggggcaggtagaaatcgacgatctcgggcagc tggeggegeageageageaegaatacetegtteagegeeaegeeeageaeggeeggetegteggeggettgeeggtataggtggagtggtagatggggttgcgccgcatggtgatgcggtccaccgtgaacaccgggaaccagtcctgc ${\tt tcgttgtagtagccggtatggtcgccataggggccttcgagcgccatttcgtagccggtggccggggcgggttg}$ geegaggeeggeacegaeaggtegetgeecagegeettgaegaeeteggtgegegageegegeageeggeg aactggtatteggacagegtgteeggeaeeggegtgaeegegeeeaggatggteggeegggteggeeeagegee acggtgatgggaaacggcttgcccgggtgggcctgggcgtggtcgcggaagtccagcgcgccccggtgcgac agccagcgcatgatcagcttgttcggccccagcggctgctgcgggtagatgcccaggttctgccgccgggcgttc ggcccgcgcgtgatcaccaggccccaggcgagcaggggcgccacgtcgcccggccagcaggtctggatgggcagg eggeteagetegaegteggegeetteeeagaegattteetggeaggeggegetgegeaeggtettggggeteatg $\verb|tcccacagggcggctttcagcatggacaccttggccagcgctcgcgcaggcccttgggcgcttcgggctcgcgc| \\$ agggaggecagcagttcgccggtttcgcgcagggcgccgacgtcgtcggcccccatgccccaggcgacccgccgc geegggeegeeggegegeageaceeggteggeaateteggteattteeageegegtegagaeeggeggtgatg cgtttgagttcgccc

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Figure 21 represents sequences amplified with molecular marker VIII (hypothetic yleA protein) in Gram-negative bacteria (SEQ ID NOs 452-461).

SEQ ID NO. 452 Haemophilus influenzae

SEQ ID NO. 453 Pasteurella multocida

ctacgcgtgataacgtcccacgccgagttcatcttctttacgagtacgattaatcaccatttgtggcgattgaac aacqcqaaqtcccatttqttcttcaqttctaacqacttcaccacqcaqtqaqttaqtaaacacatccqtqatctt qatatcaacaaacttcccaatcatatcaggcgtgcccacaaaattgacgatacgattagtttctgtacgccctgt qaqttccattaaatcttttttcqaqqqtccttccactaacacqcqctqttctqtqcctaacattqctcqactaaa ttgcgcggcttgattgttaatgcgttgttgcaacacatataaacgttgtttcttcttcttcttctgtcacatcatc aggcatatctgctgctggcgtgcctggacgtgctgaataaatgaagctgaaactcatatcaaaatttacttgtgc aattaaattcatggtttgctcgaaatcttctgctgtttcgcccgggaaaccgacaataaaatctgagctaatttg aatctctggacgcaccgctcttaacttccgaataatcgatttatattctaatgccgtatgattgcgtttcatcat agataacacacgatcagaaccactttgtacaggtaagtgtaagaaactcaccaactctggcgtatcacggtacac atcaataatgtcatcagtgaactcaattgggtgactggtgataaaacgtaaacqgtcaataccatcaatagcggc tactaaacqtaacaattccqcaaaaqtacaaataccqtcatcatqaqttqcaccacqataaqcqttcacqttttq tcctaataaattcacttcacgcacgccttgctctgccaactgtgcaatttcaaataatacatcatccactggacg qaaaqcaqttqqaccttctqcacqcqqttctqqtaaacqqtcqaatttttcaatttctqqaaaactqacatcqac tactgagettttaccacetetgatetgateattteaggtaaaegatgtaaggtttgtggteeaaaaataat atcgacataaggagcacgagtacgaatgtgttctccttcttgtgaggcaacacagcccccaacaccgataacgag teceggettatgtttetttaattettteeaaegteetaattgatggaaaaetttttettgtgettttteaegaat tgagcaagtgtttaacaataacacatccgcttcttccggaatttctgttaactctaagccgtgagtactgtttaa gagatctgccattttagatgaatcatattcattcatctgacaaccccacgttttaatatgtaattttttgcgtcat

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SEQ ID NO. 454 Haemophilus ducreyi

tcttccgctgtttcgccaggaaagccaacaatgaaatctgagctaatttggatatttggacgaaccgcacgtaat ttacgaataatggctttgtattctaatgcggtgtggttacgtttcatcatggttaaaacacgatcggcgccactt tggataggtaaatgcaagaagctgaccaattctggagtatcacgatacacttcaataatgtcgtcggtgaattca atggggtggcttgtggtataacgtaagcggtcaataccatcaatggcggcaactaaacgtaataattctgcaaaa gtgcaaatgccaccatcaaaggtttcaccacggtaagcattaacgttttgacccagcaagttaacttcacgaacg ccttgctctgctaattgtgcgatttcgaataagacatcatcaacagggcgggaaacttcttcaccacgggtataa ggcactacacagaatgagcagtatttattacagccttccataattgatacgaaagcagttggaccttctgctttg ggttctggtaagcggtcgaatttttcaatttctgggaaggagatatcgactactgcacgatcgcctgatcggatc tggttgatcatttctggtaagcggtgcaatgtttgtggcccaaatactatatcaacaaaaggggcacgttcacgg atatgttcaccttcttgtgaagcaacacagccaccaacgccaataattaaatcgggtttgtcctttttccagttt ${\tt tccgcttcttcaggtttatcggttaattctaatccgtgtgttgagtttaagagatctgccatttttgatgagtca}$ tactcattcatttggcaaccccaagttgtgatatgtaattttgccataattttcaaaaaataataatatctcaa ta agtta aaata aaagcgta aagaga cagttcccttta cgcatcttta atcgtgctattctacctgtttgcttattttttcgctagagttaatcgcttaataagcaaaatgccacgatattgctagcgtgacattttatcatgagaggat gttattgtttggttaaggtcaatacaacactttcaccggcaacaacatttccaacttttt

SEQ ID NO. 455 Vibrio parahaemolyticus

SEQ ID NO. 456 Yersinia pestis

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 $\verb|ctgttggcta| at gcgttgttgtcaggatatgtagccgctgttttttctcctcttcggacacattgttgggta| aatc$ agccgctggtgtgccgggacgcgggggagtaaataaagctgtagctggtatcaaaatgaatatctgcgaccagttt $\verb|catggtctgttcaaaatcctgctgggtttcaccagggaagccgacaataaaatcagaacttatctggatatcagg|\\$ $\tt gcgtgcttgacgcagtttgcggatgatggctttgtattccaaggcggtatgggcacgcttcatcatggtcaaaat$ $\verb|acggtcagaaccgctttgtaccggcaaatgcaggaagctcaccaattcaggcgtatcgcgataaacatcaatgat|$ atcgtcagtaaactcaatggggtggctggtggtaaatcgtaccctatcgataccatcaatcgccgcaaccaaacq $\verb|caacagctcggcaaaactacagatatcgccatcgtaggttgccccgcggtaggcgttaacattctggccgagtaa|$ $\tt gttgacttcacgtacgccttgagcggctaactgggcgatttcaaaaaagaatgtcatcgcttggacggctgacttc$ tgggccttcagcccgtggttctggcaaacggtcaaatttttcaatttcgggaaaactgatatccacgacagggct attegtteettgeaegtggttaateattteeggtaaaegatgeagegtttgtggeeegaagatgaeategaeaea gggggcgcgctggcgcaattgttcaccttcctgtgacgccacgcaaccaccgaccccaataatcaactgcgggtt tttctctttcaataatttccattgccctagcaggctgaatactttttcctgtgctttttcccggatagaacaggt $\verb|atttagcagcagtaaatccgcttcttccgggatggttaactggtagccatgggtactggccaagagatctgc|$ cattttagatgaatcgtattcattcatctggcaaccccaggttttgatatgcagttttttagtcatcgggttatt catcatcaaaatcacctcgttccgtgcggtactccgttgtggtagataatctccgttgtagtagagagtcgcaaa ggcttcgtcgttagggagcattgtagtcatttgcctctgcgatgaccaccgcagaaccgttgagttattctgttg agtgataaaaaatccgttacactgcggttagacaaaaccttgctaatg

SEQ ID NO. 457 Salmonella typhimurium

 $\tt gccqaqcatacqgcqgctccatqccatcqcctqctqattqatacqctcttqcaqaatatacaqacqctqcttctt$ ctcttcttccggcacgtcatcaaccatatcggcagccggcgttcccggacgcgcagagaagataaagctgtagct ${\tt agtgtgggtgcgccccatcagattcaacacgcgatcggaaccgctctgtaccggcagatgcaggaaactgaccag}$ $\verb|ttccggcgtatcgcggtatacctcgataatatcgtcggtgaactcaatcggatggctggtgataagcgaatacg|$ gtcaatgccgtcgatggcggcaaccagacgcagatcggcaaaggtaccggtggtgccgtcgtagttttctcc gcagccttccatgatagaaacgaaagcggtcgggccttctgcgcgcggttccggcaaacggtcgaacttctcgat $\verb|ttccgggaagctgatatcgaccaccgggctgcggtcgccaccgcacggagttaatcatctccggtaggcggtgtaa||$ ggtttgcgggccaaaataatgtcgacgtaatgggcgcgttgacgaatgtgctcgccttcctgggaagccacgca gccgccgacgccgataatcagatcgggatttttctcttttaacagtctccagcgacctaattgatggaagacttt tteetgageettetegeggattgageaggtatteaacageageacateegeetetteegeeaegteggteagttg atagccgtgggtggcgtccagcagatcggccatcttcgatgaatcgtactcgttcatctgacagccccaggtttt aatatggagttttttagtcatcgacttgctcttgcgaaatagtggctgaaaagcagggcgcatagtgtaatgctt tggcgcggttgtgaccagtatgactgacgtcagccctaatgggtaaaaaatcctgtaaaacttgtctaaaacgtaa caggatgaatgaccatgacaaatcaaccaacggaaattgccattgtcggcgggggaatggtcggcggcgctgg cgctgggtctggcgcagcaagggtttacggtgatggtaatagaacatgccgcgcctgcgccgtttgtggcggaca gccagcctgacgtgc

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SEQ ID NO. 458 Vibrio cholerae

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SEQ ID NO. 459 Escherichia coli K12

SEQ ID NO. 460 Escherichia coli 0157:H7

Catcatcaaccatatcggcggctggtgtacccggacgtgcagagaagataaagctgtagctcatgtcgaaattga cgtcggcaatcagctcatgtcgaagtcagaac

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SEQ ID NO. 461 Pseudomonas aeruginosa

 $\verb|cegccgtacggtcgtcggcctcaatgcagggtgctgtcgatcagggtaccgcgcagcgagtgcggcagcgcgtcg| \\$ $\verb|tcgatgtgcacctgggcgaactggccgatcaggcgtggattgtcgcagcggaagttgacgatccggttgttctcg| \\$ gtgcgcccctggagcatgcctgggtccttcttcgagaagtcggtgaccaggatccgctgggtgctgccgaccatg $\verb|cgccggctgatctcgtagccttgctggtggatgcggctctggaggatctgcaggcgctgtttcttcacttcttcc|\\$ ccgacgtcctccaccagcttcatggtctgctcgaagtccttctcggtttcgccggggaaaccgacgatgaagtcg gagctgatgcagatgtccggtaccgcggccttcagcttgcggatacgcgacttgtattccagcacggtatggttg $\verb|cgettcategecgecagcacgggtcggagcccgactgcaccggcaggtggatgaatttcaccagctccggcacc| \\$ $\verb|teggcgtgggcctggatcagcgcgtcggagaattccagcgggtgcgaggtggtatagcggatgcgctcgataccg|$ tegacggeggegaceaceegeageagtteggegaagteggeeaggeggeeategtgggteaggeegggaageeg $\verb|ttgacgttctgtcccagcagggtgacttcgcggacgccgttctcggccaggtggatcacttcggcgatcacgtcg|$ $\verb|tcgaatggtcggctgacttcctcgccgcgggtgtagggcaccacgcagaagctgcagtacttgctgcagccttcc||$ atcaccgagacgaaggcggtggggccatcgacccgcggttccggcaggcggtcgaatttctcgatttccgggaag gacacgtcgacctgcggcttgcgcgtgctgcggcggcgtcgatcatttccggcaggcggtgcagggtctgcggg $\verb|ccgatcaccaggtcgggattctgcttcagctcgcgccacatgccgagcttggaaaacaccttttcctgggcc|$ ttetegeggategageaggtattgageaggatgaegteggeeteggeggegtttteggteaeetegagggettgg tgttcaccgagcaggtccgccattcgcgacgagtcgtactcgttcatctggcagccgtgggtttcgatgaaaagc $\verb|ttcttggccatgcgcttcgtcggacagttcgaaaaggaccgcgcattatagagggcggggcccccggttcctagc||$ gttgctggccgaaaggctgtgctatgattcgcgcccttcattttccggcattgctttccccgccatgaacaagcg cgaaaaccccatctacaaggtgattttcctcaaccagggccaggtcttcgagatgtatgc